```
 26 TGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCT 75
    |||:::   |||||||||:::::   :::   |||   |||      ::
711 CysPheThrCysThrCysGlnLysLysThr...ValIleCysAspProVa 726

 76 CCACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAAT 125
    :   ||||||   :::   |||   :::   |||          :::||||
726 lMetCysProThrLeuSerCysThrHisThrValGlnProGluAspGlnC 743

126 GCTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCC... 172
      ||||||||   |||   |||             :::         |||
743 ysCysProIleCysGluGluLysLysGluSerLysGluThrAlaAlaVal 759

173 ..............CCACCAAAGTCCTGCCAGCACAACGGGACCATGTA 207
              |||:::::::|||      :::|||   :::
760 GluLysValGluGluAsnProGluGlyCysTyrPheGluGlyAspGlnLy 776

208 CCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCTGC 257
       :::|||:::          :::   |||   :::   |||
776 sMetHisAlaProGlyThrThrTrpHisProPheValProProPheGlyT 793

258 CCAACCAGTGTGTCCTCTGCAGCTGC......ACAGAGGGCCAGATCTAC 301
      :::|||::::::|||:::|||      :::   |||:::::::::
793 yrIleLysCysAlaValCysThrCysLysGlySerThrGlyGluValHis 809
```

FIG. 1

```
302 TGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCGCT 351
      |||      :::||||||||||          |||      |||:::
810 CysGluLysValThrCysProProLeuThrCysSerArgProIleArgAr 826

352 G...CCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAAT 398
       |||::::::||||||:::   |||      |||   :::
826 gAsnProSerAspCysCysLysGluCysProProGluGluThrProProL 843

399 CGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAG 448
                :::::::|||:::   :::|||:::
843 euGluAspGluGluMetMetGlnAla..................... 851

449 GATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCCAGC 498
                                |||||||
852 ..................................AspGlyThr..... 854

499 CCCCACTGGCCTCAGCGCCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 548

854 ..................................... 854

549 CCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACAT 598

854 ..................................... 854
```

FIG. 1 (CONT.[1])

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```
599 ANGAAAGCCTGTGTGCATGGCGGGAAGACGTACTCCCACGGGGAGGTGTG 648
      :::   |||       |||   :::   |||:::::::::::|||   ||
855 ...ArgLeuCysLysPheGlyLysAsnTyrTyrGlnAsnSerGluHisTr 870

649 GCACCCGGCCTTCCGTGCCTTCGGCCCTTGCCCATGCATCCTATGCACCT 698
    |||||||:::              |||          ||||||  |||   |
870 pHisProSerValProLeuValGlyGluMetLysCysIleThrCysTrpC 887

699 GTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACGAAGTAC 748
        ||:::   |||          |||||||||      ||||||
887 ysAspHisGlyValThrLysCysGlnArgLysGlnCysProLeu...Leu 902

749 CCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCC 798
      ||||||:::|||   ::::::   ||||||||||||      |||
903 SerCysArgAsnProIleArgThrGluGlyLysCysCysProGluCysIl 919

799 AGAGGAC 805
    ||||||
919 eGluAsp 921
```

FIG. 1 (CONT.[2])

```
863 TCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGG 912
    |||   |||      ::::::          |||      :::   :::||
  3 SerTyrHisArgSerHisTyrAspProProProSerArgGlnAlaGlyGl 19

913 GAGAAAGAGAGGCCCGGGCACCCCAGCCCCCACTGGCCTCAGCGCCCCTC 962
          |   :::|||   |||||:::   :::      |||
 19 yLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeu..... 33

963 TGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACT 1012
              :::      :::   |||:::::::|||
 34 ..................MetAspSerGlnGlnAlaSerGlyThrIle 43

1013 GTCAAGATCGTCCTG......AAGGAGAAACATANGAAAGCCTGTGTGCA 1056
      |||:::|||||||:::      |||:::||||||   ::::::||||||
  44 ValGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysValSe 60

1057 TGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTG 1106
      :::|||||||||||||||||||||||||  ||||||||   :::||||
  60 rAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuArgA 77

1107 CCTTCGGCCCTTGCCCATGCATCCTATGCACCTGTGAGGATGGCCGCCAG 1156
     ||||||||         |||:::|||||||||||||:::      :::|||
  77 laPheGlyIleValGluCysValLeuCysThrCysAsnValThrLysGln 93
```

FIG.2A

```
1157 GACTGCCAGCGTGTGACCTGTCCCACGAAGTACCCCTGCCGTCACCCCGA 1206
     :::|||:::::::::   ||||||::::::||||||||||::::::|||::
  94 GluCysLysLysIleHisCysProAsnArgTyrProCysLysTyrProGl 110

1207 GAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAAGCAGAC. 1255
       :|||:::   ||||||||||||||::||||||      ||||||
  110 nLysIleAspGlyLysCysCysLysValCysProGlyLysLysAlaLysG 127

1256 ........CCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCCAAG 1294
         ||||||::|||   :::   ::::::      |||   :::
  127 luGluLeuProGlyGlnSerPheAspAsnLysGlyTyrPheCysGlyGlu 143

1295 GCACCGGGCCGGGTCCTCGTCCACACATCGGTA...TCCCCAAGCCCAGA 1341
           :::   |||:::  ||||||         :::   ::
  144 Glu......ThrMetProValTyrGluSerValPheMetGluAspGlyGl 158

1342 CAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTCGGACTTGGTGGAGA 1391
     ::::   |||::::::|||||||||   |||              ||||||:
  158 uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175

1392 TCTACCTCTGGAAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNNNN 1441
                     :::::::::|||   :::
  175 alHisValTrpThrIle..................................... 180
```

FIG.2A (CONT.[1])

```
1442 NNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGAATTTCCACTTGACTCAGAT 1491
                  |||:::||||||          ||
 181 ............ArgLysGlyIleLeuGlnHisPheHis.........Il 190

1492 CAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGAC 1541
     |:::|||:::   |||:::   |||:::   |||       ||||||:::|
 190 eGluLysIleSerLysArgMetPheGlu...GluLeuProHisPheLysL 206

1542 TGCTCGCTGGCCCCCACGAAGGTCACTGGAACGTCTTCCTAGCCCAGACC 1591
           ||::::::              ::::::|||::::::|||
 206 euValThrArgThrThrLeuSerGlnTrpLysIlePheThrGluGlyGlu 222

1592 CTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACA 1641
        :::::::::      :::|||                      +++
 223 AlaGlnIleSerGlnMetCysSer.......................... 230

1642 AAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATAT 1691
         :::   ||||||   ||||||   :::              :::
 231 ....SerArgValCysArgThrGluLeuGluAspLeuValLysValLeuT 246

1692 TAATAAATAAGAAGTTGCATAACCAT 1717
      ::::::::::::      :::|||
 246 yrLeuGluArgSerGluLysGlyHis 254
```

FIG.2A (CONT.[2])

```
100 TCTTCCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCCTGCCCACCGCTG 149
    :::::::|||||   |||     |||::::  |||::::  |||
429 ThrAlaHisLeuLeuGlyPro.....ProGlyThrProGlyProArg.. 442

150 CTTCCTGGCCCCCGACCCCCGCTCTAGCAGCAGACCTCCTGGGGTCA 199
        |||||||  ::::|||::::     |||||||:
443 .......ArgLeuLysGlyPheTyrGlySerGluAlaGlnGlyValV 457

200 TGTGGGTTGATCTGTGGCCCCCTGTGNCTCCGTGTCCTTTTTCGTCTCCCGT 249
        ::       |||||||  |||     |||||||  |||
457 al...LysAspLeuGluProGluLeuLeuArgHisLeu..........  468

250 CCTCCCCGACTCTCCGCTCCCGGACCAGCGGCCCTGACCCTGGGGAAGGATGG 299
        |||     |||:::+++          ||
469 .........AlaLysGlyMetAlaSerLeuLeuIleThrThrLysGl 481

300 TTCC...CGAGGTGAG.....................................
    ||||    |||||||||
481 ySerProArgGlyGluLeuArgGlyGlnValHisIleAlaAsnGlnCysG
```

FIG. 2B

```
313 .....GGTCCTCTCCTCCTT..............GCTGGGACTCGCGCT 342
      |||   |||   |||                  |||:::||||||
498 luValGlyGlyLeuArgLeuGluAlaAlaGlyAlaGluGlyValArgAla 514

342 ..................................................  342

515 LeuGlyAlaProAspProAlaSerAlaAlaProProValValProGlyLe 531

343 ....GCTCTGGTTCCC......CCTGGACTCCCACGCTCGAGCCCGCCCA 382
       ||||||:::|||      ||||||   ||| :::|||   |||
531 uProAlaLeuAlaProAlaLysProGlyGlyPro.GlyArgProArgAsp 547

383 GACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTG 432
        |||:::|||:::|||::::::         |||     ||
548 ProAsnThrCysPhePheGluGlyGlnGlnArgProHisGlyAlaArgTr 564

433 GCACCCCTACTTGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCT 482
    |   |||      :::|||                |||    ||||||
564 pAlaProAsnTyrAspPro.............LeuCysSerLeuCysThrC 577
```

FIG. 2B (CONT.[1])

```
483 GCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTC 532
    ||:::::::   :::   |||  |||       :::   |||||||||
577 ysGlnArgArgThr...ValIleCysAspProValValCysProProPro 592

533 CACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGT 582
    ||||||:::||||||      |||:::|||||||||||||   |||
593 SerCysProHisProValGlnAlaProAspGlnCysCysProValCysPr 609

583 GGAA.....CCTCACACTCCCTCTGGACTCCGGG 611
    |||          |||      |||   :::   |||
609 oGluLysGlnAspValArgAspLeuProGlyLeuProArgSer...ArgA 625

612 CCCCACCAAAGTCCTGCCAGCACAACGGGACCATGTACCAACACGGAGAG 661
      |||   :::::::|||      :::|||                :::::::
625 spProGlyGluGlyCysTyrPheAspGlyAspArgSerTrpArgAlaAla 641

662 ATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCTGCCCAACCAGTGTGT 711
        |||   :::   |||                 :::|||::
642 GlyThrArgTrpHisProValValProProPheGlyLeuIleLysCysAl 658

712 CCTCTGCAGCTGCACA......GAGGGCCAGATCTACTGCGGCCTCACAA 755
    ::::|||:::|||            |||::::::::::|||     :::
658 aValCysThrCysLysGlyGlyThrGlyGluValHisCysGluLysValG 675
```

FIG. 2B (CONT.[2])

```
756 CCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCGCTG...CCAGACTCC 802
     ||||||:::   :::|||      |||:::   :::   |||   :::
675 lnCysProArgLeuAlaCysAlaGlnProValArgValAsnProThrAsp 691

803 TGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGA 852
                    ||||||:::   |||
692 CysCysLysGlnCys..................................... 696

853 CAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAG......GATCCAT 896
          :::   :::     |||||||||     ||||||
697 ..........ProValGlySerGlyAlaHisProGlnLeuGlyAspProM 710

897 GTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCCAGCCCCCACT 946
                :::::|||                |||||
710 etGlnAlaAsp..............GlyPro..................... 715

947 GGCCTCAGCGCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGG 996

715 ..................................................... 715

997 AGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATANGAAAG 1046
                                :::::
716 ..........................................ArgG 717
```

FIG. 2B (CONT.[3])

```
1047 CCTGTGTGCATGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCG 1096
     ::|||      :::|||:::   :::   :::::::::   |||||||||
 717 lyCysArgPheAlaGlyGlnTrpPheProGluSerGlnSerTrpHisPro 733

1097 GCCTTCCGTGCCTTCGGCCCTTGCCCATGCATCCTATGCACCTGTGAGGA 1146
       :::          ||||||          ||||||   |||   |||
 734 SerValProProPheGlyGluMetSerCysIleThrCysArgCysGlyAl 750

1147 TGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACGAAGTACCCCTGCC 1196
      |||         |||:::|||      |||                |||
 750 aGlyValProHisCysGluArgAspAspCysSerLeuProLeuSerCysG 767

1197 GTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGC..... 1237
           ::::::      ::::::|||||||::   |||
 767 lySerGlyLysGlu.....SerArgCysCysSerArgCysThrAlaHis 781

1238 .............CCAGAGGACAAAGCAGACCCT 1258
               ||||||   ::::::||||||
 782 ArgArgProAlaProGluThrArgThrAspPro 792
```

FIG. 2B (CONT.[4])

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```
  3 CTTCCCCCTTTCTTTGATCGCCTCTCC.............CTTCTGCTGGA 40
    |||||||||      ::::::   :::              |||   |||||
540 LeuProProValArgSerGlnAlaAlaGlyHisAlaTrpLeuSerLeuAs 556

 41 CCTTCCTTCGTCTCTCCATCTCTCCCTCCTT...................T 72
    |             ||||||   :::::::|||                   |
556 pThrHisCysHisLeuHisTyrGluValLeuLeuAlaGlyLeuGlyGlyS 573

 73 CCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTT 122
        ||   ::::::      |||                    +++
573 erGluGlnGlyThrValThr.............................. 579

123 CCTGCCCTCCTTTCCTGCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCC 172
       |||   |||      ||||||   :::||||||||||::: |||
580 ...AlaHisLeuLeuGlyProProGlyMetProGlyProGln.ArgLeuL 595

173 GCTCT.........AGCAGCAGACCTCCTGGGGTCATGTGGGTTGATCTG 213
     :::          :::|||:::      |||||||:::      ||||||
595 euLysGlyPheTyrGlySerGluAlaGlnGlyValVal...LysAspLeu 610

214 TGGCCCCTGTGNCTCCGT.............................GT 233
     |||:::   ||||||                                ::
611 GluProValLeuLeuArgHisLeuAlaGlnGlyThrAlaSerLeuLeuIl 627
```

Fig. 2C

```
234 CCTTTTCGTCTCCCGTCCTCCCGACTCCGCTCCCGGACCA..... 273
          :          |||   |||      :::      |||
627 eThrThrLysSerSerProArgGlyGluLeuArgGlyGlnValHisIleA 644

274 .....GCGGCC 279
                :::
644 laSerGlnCysGluAlaGlyGlyLeuArgLeuAlaSerGluGlyValGln 660

280 TGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCCTCTCCTCCTTGC 329
    +++|||   :::   :::|||:::   :::   :::|||:::|||   ||
661 MetProLeuAlaProAsnGlyGluAlaAlaThrSerProMetLeuProAl 677

330 TGGGACT...CGCGCTGCTCTGGTTCCCCCT......GGACTCCCACGCT 370
    ||||          |||   ||||||          |||   ||| :::
677 aGlyProGlyProGluAlaProValProAlaLysHisGlySerPro.Gly 693

371 CGAGCCCGCCCAGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCC 420
       |||   |||            |||:::|||:::|||::::::
694 ArgProArgAspProAsnThrCysPhePheGluGlyGlnGlnArgProHi 710

421 CGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGTACTGCC 470
     |||      |||   |||      :::|||                |||
710 sGlyAlaArgTrpAlaProAsnTyrAspPro.....LeuCysS 723
```

FIG. 2C (CONT.[1])

```
471 TGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCAC 520
        |||   |||::::::   :::   |||   |||      :::
723 erLeuCysIleCysGlnArgArgThr...ValIleCysAspProValVal 738

521 TGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTG 570
    |||||||||     ||||||:::||||||         :::|||||||||
739 CysProProProSerCysProHisProValGlnAlaLeuAspGlnCysCy 755

571 TCCCAAGTGTGTGGAA.....................CCTCACACTCCCT 599
    ||||   |||   |||                     |||      |||:
755 sProValCysProGluLysGlnArgSerArgAspLeuProSerLeuProA 772

600 CTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATGTAC 649
        ::             |||   :::::::|||      :::|||
772 sn......LeuGluProGlyGluGlyCysTyrPheAspGlyAspArgSer 786

650 CAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCTGCC 699
          ::::::                 |||   :::   |||
787 TrpArgAlaAlaGlyThrArgTrpHisProValValProProPheGlyLe 803

700 CAACCAGTGTGTCCTCTGCAGCTGC......ACAGAGGGCCAGATCTACT 743
      :::|||::::::|||:::|||      :::   |||:::::::::|
803 uIleLysCysAlaValCysThrCysLysGlyAlaThrGlyGluValHisC 820
```

FIG. 2C (CONT.[2])

```
744 GCGGCCTCACAACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCGCTG 793
      ||       :::   ||||||:::   :::|||       |||:::
820 ysGluLysValGlnCysProArgLeuAlaCysAlaGlnProValArgAla 836

794 ...CCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATC 840
                |||   :::|||||||:::   |||
837 AsnProThrAspCysCysLysGlnCys..................... 845

841 GGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGG 890

845 ..................................................... 845

891 ATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCCAGCC 940
                              |||:::
846 .....................................ProVal 847

941 CCCACTGGCCTCAGCGCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACC 990
     :::|||   :::|||   |||:::         :::          ||
848 GlySerGlyThrAsnAlaLysLeuGlyAspProMetGlnAlaAspGlyPr 864

991 CAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATA 1040
                            |:::|||
864 oArgGly.................................... 866
```

FIG. 2C (CONT.[3])

```
1041 NGAAAGCCTGTGTGCATGGCGGGAAGACGTACTCCCACGGGGAGGTGTGG 1090
         |||      :::|||:::   :::   :::::::::   |||
 867 ........CysArgPheAlaGlyGlnTrpPheProGluAsnGlnSerTrp 880

1091 CACCCGGCCTTCCGTGCCTTCGGCCCTTGCCCATGCATCCTATGCACCTG 1140
     ||||||:::         ||||||         ||||||   |||   ||
 881 HisProSerValProProPheGlyGluMetSerCysIleThrCysArgCy 897

1141 TGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACGAAGTACC 1190
            |      |||         |||:::|||      |||
 897 sGlyAlaGlyValProHisCysGluArgAspAspCysSerProProLeuS 914

1191 CCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGC... 1237
       |||         ::::::     ::::::||||||:::   |||
 914 erCysGlySerGlyLysGlu......SerArgCysCysSerHisCysThr 928

1238 ............................CCAGAGGACAAAGCAGACCC 1257
                     ||||||   :::   :::
 929 AlaGlnArgSerSerGluThrArgThrLeuProGluLeuGluLysGluAl 945

1258 TGGCCACAGT 1267
     ||||||
 945 aGluHisSer 948
```

FIG. 2C (CONT.[4])

```
656 TCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGG 705
    |||   |||      ::::::          |||      :::   :::||
  3 SerTyrHisArgSerHisTyrAspProProProSerArgGlnAlaGlyGl 19

706 GAGAAAGAGAGGCCCGGGCACCCCAGCCCCCACTGGCCTCAGCGCCCCTC 755
          |   :::|||   |||||:::   :::      |||
 19 yLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeu..... 33

756 TGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACT 805
              :::      :::   |||::::::|||
 34 .....MetAspSerGlnGlnAlaSerGlyThrIle 43

806 GTCAAGATCGTCCTG......AAGGAGAAACATANGAAAGCCTGTGTGCA 849
     |||:::|||||||:::      |||:::||||||   ::::::||||||
 44 ValGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysValSe 60

850 TGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTG 899
    :::||||||||||||||||||||||||  ||||||||   :::||||
 60 rAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuArgA 77
```

FIG. 3A

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```
900 CCTTCGGCCCTTGCCCATGCATCCTATGCACCTGTGAGGATGGCCGCCAG 949
    |||||||         |||:::|||||||||||||:::      :::|||
 77 laPheGlyIleValGluCysValLeuCysThrCysAsnValThrLysGln 93

950 GACTGCCAGCGTGTGACCTGTCCCACGAAGTACCCCTGCCGTCACCCCGA 999
    :::|||:::::::::   ||||||::::::||||||||:::::|||::
 94 GluCysLysLysIleHisCysProAsnArgTyrProCysLysTyrProGl 110

1000 GAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAAGCAGAC. 1048
       :|||:::   ||||||||||||||::||||||      ||||||
 110 nLysIleAspGlyLysCysCysLysValCysProGlyLysLysAlaLysG 127

1049 ........CCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCCAAG 1087
         ||||||:::|||   :::   ::::::      |||   :::
 127 luGluLeuProGlyGlnSerPheAspAsnLysGlyTyrPheCysGlyGlu 143

1088 GCACCGGGCCGGGTCCTCGTCCACACATCGGTA...TCCCCAAGCCCAGA 1134
           :::   |||:::   ||||||          :::   ::
 144 Glu......ThrMetProValTyrGluSerValPheMetGluAspGlyGl 158
```

FIG. 3A (CONT.[1])

```
1135 CAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTCGGACTTGGTGGAGA 1184
     ::::   |||::::::|||||||||   |||              ||||||:
 158 uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175
1185 TCTACCTCTGGAAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNNNN 1234
                     ::::::::|||   :::
 175 alHisValTrpThrIle..................................  180

1235 NNNNNNNNNNNNNNNNNNNNNNNNNNNCAGAATTTCCACTTGACTCAGAT 1284
                  |||::::||||||        ||
 181 ............ArgLysGlyIleLeuGlnHisPheHis.........Il 190

1285 CAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGAC 1334
     |:::|||:::   |||:::   |||:::   |||      ||||||:::|
 190 eGluLysIleSerLysArgMetPheGlu...GluLeuProHisPheLysL 206

1335 TGCTCGCTGGCCCCCACGAAGGTCACTGGAACGTCTTCCTAGCCCAGACC 1384
          ||::::::              ::::::|||::::::|||
 206 euValThrArgThrThrLeuSerGlnTrpLysIlePheThrGluGlyGlu 222

1385 CTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACA 1434
        :::::::::      :::|||                    +++
 223 AlaGlnIleSerGlnMetCysSer.........................  230
```

FIG. 3A (CONT.[2])

```
1435 AAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATA 1484
       :::  ||||||||  :::          :::
231 ....SerArgValCysArgThrGluLeuGluAspLeuValLysValIL 246

1485 TAATAAATAAGAAGTTGCATAACCAT 1510
       :::::::::::  :::|||
246 yrLeuGluArgSerGluLysGlyHis 254
```

FIG. 3A (CONT.[3])

```
368 CCCACTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCA......CC 411
    |||::::::   |||      |||:::|||          |||      ||
532 ProAlaLeuAlaProAlaLysProGlyGlyProGlyArgProArgAspPr 548

412 AAAGTCCTGCCAGCACAACGGGACCATGTACCAACACGGAGAGATCTTCA 461
    |:::::::||      :::|||   :::     ||||||      ::::
548 oAsnThrCysPhePheGluGlyGlnGlnArgProHisGlyAlaArgTrpA 565

462 GTGCCCATGAGCTGTTCCCCTCCCGCCTGCCCAACCAG.........TGT 502
    ::                              ||||||          |||
565 la.............................ProAsnTyrAspProLeuCys 572

503 GTCCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAACCTG 552
     ||||||:::|||   :::      :::   |||      ::::::||
573 SerLeuCysThrCysGlnArgArgThrValIleCysAspProValValCy 589

553 CCCCGAACCAGGCTGCCCAGCACCCCTCCCGCTGCCAGACTCCTGCTGCC 602
    ||||   |||::::||||||   |||:::      ||||||:::|||||||
589 sProProProSerCysProHisProValGlnAlaProAspGlnCysCysP 606

603 AAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTG 652
     :::|||                            |||::::::::::|||
606 roValCys.........................ProGluLysGlnAspVal 614
```

FIG. 3B

```
653 CAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCA.........TGTTC 693
     :::::::|||   |||:::   :::   :::||||||          |||
615 ArgAspLeuProGlyLeuProArgSerArgAspProGlyGluGlyCysTy 631

694 CAGTGATGCTGGGAGAAAG...AGAGGCCCGGGCACC..............  727
          |||:::   |||:::   |||:::   ||||||
631 rPheAspGlyAspArgSerTrpArgAlaAlaGlyThrArgTrpHisProV 648

728 ..CCAGCCCCCACTGGCCTC.............................  745
                      |||   ||||||
648 alValProProPheGlyLeuIleLysCysAlaValCysThrCysLysGly 664

745 .............................................  745

665 GlyThrGlyGluValHisCysGluLysValGlnCysProArgLeuAlaCy 681

746 .AGCGCCCCTCTGAGCTTCATCCCTCGCCACTTC.........AGACCCA 785
     :::   |||:::         |||                    |||
681 sAlaGlnProValArgValAsnProThrAspCysCysLysGlnCysProV 698
```

FIG. 3B (CONT.[1])

```
786 AGGGAGCAGGCAGC...ACAACTGTCAAGATCGTCCTGAAGGAGAAACAT 832
        |||:::|||:::         :::         ::::::
698 alGlySerGlyAlaHisProGlnLeuGlyAspProMetGlnAlaAspGly 714

833 ANGAAAGCCTGTGTGCATGGCGGGAAGACGTACTCCCACGGGGAGGTGTG 882
     :::::::|||      :::|||:::   :::   :::::::::   ||
715 ProArgGlyCysArgPheAlaGlyGlnTrpPheProGluSerGlnSerTr 731

883 GCACCCGGCCTTCCGTGCCTTCGGCCCTTGCCCATGCATCCTATGCACCT 932
    |||||||:::         ||||||         ||||||  |||   |
731 pHisProSerValProProPheGlyGluMetSerCysIleThrCysArgC 748

933 GTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACGAAGTAC 982
          ||     |||         |||:::|||      |||
748 ysGlyAlaGlyValProHisCysGluArgAspAspCysSerLeuProLeu 764

983 CCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGC.. 1030
      |||         ::::::     ::::::||||||:::   |||
765 SerCysGlySerGlyLysGlu......SerArgCysCysSerArgCysTh 779

1031 ..................CCAGAGGACAAAGCAGACCCT 1051
                  ||||||   ::::::||||||
 779 rAlaHisArgArgProAlaProGluThrArgThrAspPro 792
```

FIG. 3B (CONT.[2])

```
1031 TCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGG 1080
     |||   |||      ::::::          |||      :::   :::||
   3 SerTyrHisArgSerHisTyrAspProProProSerArgGlnAlaGlyGl 19

1081 GAGAAAGAGAGGCCCGGGCACCCCAGCCCCCACTGGCCTCAGCGCCCCTC 1130
           |   :::|||   ||||||:::   :::      |||
  19 yLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeu..... 33

1131 TGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACT 1180
                :::      :::   |||:::::::|||
  34 .....MetAspSerGlnGlnAlaSerGlyThrIle 43

1181 GTCAAGATCGTCCTG......AAGGAGAAACATANGAAAGCCTGTGTGCA 1224
      |||:::||||||:::      |||:::||||||   ::::::||||||
  44 ValGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysValSe 60

1225 TGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTG 1274
      :::|||||||||||||||||||||||  ||||||||   :::||||
  60 rAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuArgA 77
```

FIG. 4A

```
1275 CCTTCGGCCCTTGCCCATGCATCCTATGCACCTGTGAGGATGGCCGCCAG 1324
     ||||||||         |||:::|||||||||||||:::      :::|||
  77 laPheGlyIleValGluCysValLeuCysThrCysAsnValThrLysGln 93

1325 GACTGCCAGCGTGTGACCTGTCCCACGAAGTACCCCTGCCGTCACCCCGA 1374
     :::|||:::::::::  ||||||:::::||||||||||:::::|||::
  94 GluCysLysLysIleHisCysProAsnArgTyrProCysLysTyrProGl 110

1375 GAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAAGCAGAC. 1423
       :|||:::   ||||||||||||||::|||||      ||||||
 110 nLysIleAspGlyLysCysCysLysValCysProGlyLysLysAlaLysG 127

1424 .........CCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCCAAG 1462
         ||||||:::|||   :::   ::::::      |||   :::
 127 luGluLeuProGlyGlnSerPheAspAsnLysGlyTyrPheCysGlyGlu 143

1463 GCACCGGGCCGGGTCCTCGTCCACACATCGGTA...TCCCCAAGCCCAGA 1509
           :::   |||:::   ||||||         :::   ::
 144 Glu......ThrMetProValTyrGluSerValPheMetGluAspGlyGl 158
```

FIG. 4A (CONT.[1])

```
1510 CAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTCGGACTTGGTGGAGA 1559
     ::::   |||::::::|||||||||   |||             ||||||:
 158 uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175

1560 TCTACCTCTGGAAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNNNN 1609
                     ::::::::|||   :::
 175 alHisValTrpThrIle.............................. 180

1610 NNNNNNNNNNNNNNNNNNNNNNNNNNNCAGAATTTCCACTTGACTCAGAT 1659
                   |||:::||||||        ||
 181 ............ArgLysGlyIleLeuGlnHisPheHis.........Il 190

1660 CAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGAC 1709
     |:::|||:::   |||:::   |||:::   |||      ||||||:::|
 190 eGluLysIleSerLysArgMetPheGlu...GluLeuProHisPheLysL 206

1710 TGCTCGCTGGCCCCCACGAAGGTCACTGGAACGTCTTCCTAGCCCAGACC 1759
           ||::::::             ::::::||:::::::|||
 206 euValThrArgThrThrLeuSerGlnTrpLysIlePheThrGluGlyGlu 222
```

FIG. 4A (CONT.[2])

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```
1760 CTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACA 1809
        :::::::::         :::|||                     +++
 223 AlaGlnIleSerGlnMetCysSer.......................... 230

1810 AAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATAT 1859
        :::   ||||||   ||||||   :::              :::
 231 ....SerArgValCysArgThrGluLeuGluAspLeuValLysValLeuT 246

            1860 TAATAAATAAGAAGTTGCATAACCAT 1885
                   ::::::::::::      :::|||
             246 yrLeuGluArgSerGluLysGlyHis 254
```

FIG. 4A (CONT.[3])

```
560 TGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTA 609
     |||:::|||:::||.|:::::::::::::   |||:::::::|||   |||
691 CysPhePheGluGlyGluGlnHisThrHisGlySerGlnTrpThrProGl 707

610 CTTGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGG 659
      :::                      |||:::   |||||||||:::::
707 nTyrAsnThr..............CysPheThrCysThrCysGlnLysL 719

660 GCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCC 709
      :::   |||   |||      :::   ||||||   :::   |||
719 ysThr...ValIleCysAspProValMetCysProThrLeuSerCysThr 734

710 CAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCA 759
      :::   |||         :::||||||||||||   |||   |||
735 HisThrValGlnProGluAspGlnCysCysProIleCysGluGluLysLy 751

760 CACTCCCTCTGGACTCCGGGCC.................CCACCAAAGT 791
      :::         |||              .          |||::::
751 sGluSerLysGluThrAlaAlaValGluLysValGluGluAsnProGluG 768
```

FIG. 4B

```
792 CCTGCCAGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCC 841
      ::|||       :::|||   :::   :::|||:::           :::
768 lyCysTyrPheGluGlyAspGlnLysMetHisAlaProGlyThrThrTrp 784

842 CATGAGCTGTTCCCCTCCCGCCTGCCCAACCAGTGTGTCCTCTGCAGCTG 891
    |||   :::   |||                 :::|||::::::|||:::||
785 HisProPheValProProPheGlyTyrIleLysCysAlaValCysThrCy 801

892 C......ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAAC 935
      |      :::   |||:::::::::|||      :::||||||||||
801 sLysGlySerThrGlyGluValHisCysGluLysValThrCysProProL 818

936 CAGGCTGCCCAGCACCCCTCCCGCTG...CCAGACTCCTGCTGCCAAGCC 982
       |||      |||:::          |||:::::::|||||||:::
818 euThrCysSerArgProIleArgArgAsnProSerAspCysCysLysGlu 834

983 TGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTC 1032
    |||      |||   :::          ::::::|||:::   :::|||::
835 CysProProGluGluThrProProLeuGluAspGluGluMetMetGlnAl 851
```

FIG. 4B (CONT.[1])

```
1033 GCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGA 1082
                                    :
 851 a..................................................  851

1083 GAAAGAGAGGCCCGGGCACCCCAGCCCCCACTGGCCTCAGCGCCCCTCTG 1132
                                  ||||||
 852 ..........AspGlyThr.....................................  854

1133 AGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACTGT 1182

 854 ..................................................  854

1183 CAAGATCGTCCTGAAGGAGAAACATANGAAAGCCTGTGTGCATGGCGGGA 1232
                   :::   |||      |||   :
 855 ..........................ArgLeuCysLysPheGlyLysA 862

1233 AGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC 1282
     ::   |||::::::::::|||   |||||||||:::            |||
 862 snTyrTyrGlnAsnSerGluHisTrpHisProSerValProLeuValGly 878
```

FIG. 4B (CONT.[2])

```
1283 CCTTGCCCATGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCA 1332
          ||||||   |||   |||:::   |||         |||||
 879 GluMetLysCysIleThrCysTrpCysAspHisGlyValThrLysCysGl 895

1333 GCGTGTGACCTGTCCCACGAAGTACCCCTGCCGTCACCCCGAGAAAGTGG 1382
      ||||      ||||||            ||||||:::|||   ::::::
 895 nArgLysGlnCysProLeu...LeuSerCysArgAsnProIleArgThrG 911

         1383 CTGGGAAGTGCTGCAAGATTTGCCCAGAGGAC 1414
                ||||||||||||      |||  ||||||
          911 luGlyLysCysCysProGluCysIleGluAsp
```

FIG. 4B (CONT.[3])

```
560 TGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTA 609
     |||   |||:::|||:::      :::   |||:::   |||   |||
693 CysSerPheGluGlyGlnLeuArgAlaHisGlySerArgTrpAlaProAs 709

610 CTTGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGG 659
      :::   :::            |||      |||:::|||::::::
709 pTyrAspArgLys..........CysSerValCysSerCysGlnLysA 722

660 GCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCC 709
      :::   |||   |||      :::   |||||||||:::::|||
722 rgThr...ValIleCysAspProIleValCysProProLeuAsnCysSer 737

710 CAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCA 759
      |||||||||      |||:::|||||||||||||   |||   |||
738 GlnProValHisLeuProAspGlnCysCysProValCysGluGluLysLy 754

760 CACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAACGGGA 809
          ::::::   |||   ::::::          :::|||
754 sGluMetArgGluValLysLysProGluArgAlaArgThrSerGluGlyC 771
```

FIG. 4C

```
810 CCATGTACCAACACGGAGAGATCTTCAGTGCC..............CAT 844
     :::::::::      :::   :::::::|||                |||
771 ysPhePheAspGlyAspArgSerTrpLysAlaAlaGlyThrArgTrpHis 787

845 GAGCTGTTCCCCTCCCGCCTGCCCAACCAGTGTGTCCTCTGCAGCTGC.. 892
      :::   |||                 :::|||::::::|||:::|||
788 ProPheValProProPheGlyLeuIleLysCysAlaIleCysThrCysLy 804

893 ....ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAG 938
      :::   |||::::::::::|||      :::||||||||||:::   :
804 sGlySerThrGlyGluValHisCysGluLysValThrCysProLysLeuS 821

939 GCTGCCCAGCACCCCTCCCGCTG...CCAGACTCCTGCTGCCAAGCCTGC 985
    ::|||      |||:::          |||::::::||||||:::   |||
821 erCysThrAsnProIleArgAlaAsnProSerAspCysCysLysGlnCys 837

986 AAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCT 1035
        |||      :::      :::    . ||||||::||||||
838 ProValGluGluArgSerProMetGluLeuAlaAspSerMetGlnSer.. 853
```

FIG. 4C (CONT.[1])

```
1036 CCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAA 1085

 853 ..................................................  853

1086 AGAGAGGCCCGGGCACCCCAGCCCCCACTGGCCTCAGCGCCCCTCTGAGC 1135

 853 ..................................................  853

1136 TTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACTGTCAA 1185
                          ||||||||||||
 854 ........................AspGlyAlaGlySer.............  858

1186 GATCGTCCTGAAGGAGAAACATANGAAAGCCTGTGTGCATGGCGGGAAGA 1235
                            |||     ||||
 859 ..............................CysArgPheGlyArgHisT  865

1236 CGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCT 1285
       |||   :::   |||   |||||||||:::           ||||||
 865 rpTyrProAsnHisGluArgTrpHisProThrValProProPheGlyGlu  881

1286 TGCCCATGCATCCTATGCACCTGTGAGGATGGC..............CG 1320
        |||:::   ||||||||   :::|||                  ||
 882 MetLysCysValThrCysThrCysAlaGluGlyIleThrGlnCysArgAr  898
```

FIG. 4C (CONT.[2])

```
1321 CCAGGACTGCCAGCGTGTGACCTGTCCCACGAAGTACCCCTGCCGTCACC 1370
              ||||:::|||      :::||||||   |||
 898 gGlnGluCysThrGlyThrThrCysGlyThr..................  908

1371 CCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAAGCA 1420
        :::         :::||||||      |||   :::   :::
 909 ..GlySerLysArgAspArgCysCysThrLysCysLysAspAlaAsnGln 924

 1421 GACCCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCC 1459
      |||      ::::::   :::   ::::::||||||   |||
  925 AspGluAspGluLysValLysSerAspGluThrArgThrPro 938
```

FIG. 4C (CONT.[3])

```
536 GGTTTGCCAGGCCCAGACATGTTCTGCCTTTTCCATGGGAAGAGATACTC 585
      |||   |||                  |||:::|||:::|||::::::
543 GlyArgProArgAspProAsnThrCysPhePheGluGlyGlnGlnArgPr 559

586 CCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGTACT 635
      |||      |||   |||      :::|||                 |
559 oHisGlyAlaArgTrpAlaProAsnTyrAspPro.............LeuC 572

636 GCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTC 685
    ||      ||||||||:::::   :::   |||   |||      :::
572 ysSerLeuCysThrCysGlnArgArgThr...ValIleCysAspProVal 587

686 CACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG 735
      |||||||||      ||||||:::||||||      |||:::|||||
588 ValCysProProProSerCysProHisProValGlnAlaProAspGlnCy 604

736 CTGTCCCAAGTGTGTGGAA.....................CCTCACACTC 764
    |||||||   |||   |||                     |||      |
604 sCysProValCysProGluLysGlnAspValArgAspLeuProGlyLeuP 621
```

FIG. 4D

```
765 CCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATG 814
      ||   :::   |||   |||   :::::::|||       :::|||
621 roArgSer...ArgAspProGlyGluGlyCysTyrPheAspGlyAspArg 636

815 TACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCT 864
        ::::::                    |||   :::   |||
637 SerTrpArgAlaAlaGlyThrArgTrpHisProValValProProPheGl 653

865 GCCCAACCAGTGTGTCCTCTGCAGCTGCACA......GAGGGCCAGATCT 908
     :::|||::::::|||:::|||                |||:::::::
653 yLeuIleLysCysAlaValCysThrCysLysGlyGlyThrGlyGluValH 670

909 ACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCG 958
     ::|||      :::   ||||||:::   :::|||       |||:::
670 isCysGluLysValGlnCysProArgLeuAlaCysAlaGlnProValArg 686

959 CTG...CCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCA 1005
             :::   |||   :::|||||||:::   |||
687 ValAsnProThrAspCysCysLysGlnCys..................... 696
```

FIG. 4D (CONT.[1])

```
1006 ATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTC 1055
                  :::   :::      |||||||
 697 ........................ProValGlySerGlyAlaHisProG 705

1056 AG......GATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGC 1099
       ||      ||||||   :::::::|||                |||||
 705 lnLeuGlyAspProMetGlnAlaAsp..............GlyPro... 715

1100 ACCCCAGCCCCCACTGGCCTCAGCGCCCCTCTGAGCTTCATCCCTCGCCA 1149

 715 ..................................................  715

1150 CTTCAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGG 1199

 715 ..................................................  715

1200 AGAAACATANGAAAGCCTGTGTGCATGGCGGGAAGACGTACTCCCACGGG 1249
           :::::::|||      :::|||:::   :::   ::::::
 716 ...........ArgGlyCysArgPheAlaGlyGlnTrpPheProGluSer 728

1250 GAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCTTGCCCATGCATCCT 1299
       :::   ||||||||||:::          ||||||          ||||||
 729 GlnSerTrpHisProSerValProProPheGlyGluMetSerCysIleTh 745
```

FIG. 4D (CONT.[2])

```
1300 ATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCA 1349
        |||    |||        |||           |||:::|||      |||
 745 rCysArgCysGlyAlaGlyValProHisCysGluArgAspAspCysSerL 762

1350 CGAAGTACCCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAG 1399
           |||          ::::::       ::::::|||||||:::
 762 euProLeuSerCysGlySerGlyLysGlu......SerArgCysCysSer 776

1400 ATTTGC.....................CCAGAGGACAAAGCAGACCCT 1426
       |||                       ||||||    ::::::||||||
 777 ArgCysThrAlaHisArgArgProAlaProGluThrArgThrAspPro 792
```

FIG. 4D (CONT.[3])

```
chordin_ed7       SPLPSAGPSF VSPSLPPFPA FSFHLSLLPT LDLPSCPPFL PTAASWPFSD
chordin_ed6TR_2   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
chordin_ed6TR_1   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

                  51                                                  100
     chordin_ed7  PALAADLLGS CGLICGPCXS VSFSSPVLPT PLPDQRPDPG ERMVPEVRVL
chordin_ed6TR_2   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
chordin_ed6TR_1   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

                  101                                                 150
     chordin_ed7  SSLLGLALLW FPLDSHARAR PDMFCLFHGK RYSPGESWHP YLEPQGLMYC
chordin_ed6TR_2   DRVFGLEPPG TNMALVGLPG PDMFCLFHGK RYSPGESWHP YLEPQGLMYC
chordin_ed6TR_1   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

                  151                                                 200
     chordin_ed7  LRCTCSEGAH VSCYRLHCPP VHCPQPVTE. PQQCCPK.CV EPHTPSGLRA
chordin_ed6TR_2   LRCTCSEGAH VSCYRLHCPP VHCPQPVTE. PQQCCPK.CV EPHTPSGLRA
chordin_ed6TR_1   ~~~ISSWGQM QNHQKSGLVN FSKDSHETSF SSSSCPSPTV EPHTPSGLRA
```

FIG. 5

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```
                    201                                                 250
     chordin_ed7    PPKSCQHNGT MYQHGEIFSA HELFPSRLPN QCVLCSCTEG QIYCGLTTCP
chordin_ed6TR_2     PPKSCQHNGT MYQHGEIFSA HELFPSRLPN QCVLCSCTEG QIYCGLTTCP
chordin_ed6TR_1     PPKSCQHNGT MYQHGEIFSA HELFPSRLPN QCVLCSCTEG QIYCGLTTCP

                    251                                                 300
     chordin_ed7    EPGCPAPLPL PDSCCQACKD EASEQSDEED SVQSLHGVRH PQDPCSSDAG
chordin_ed6TR_2     EPGCPAPLPL PDSCCQACKD EASEQSDEED SVQSLHGVRH PQDPCSSDAG
chordin_ed6TR_1     EPGCPAPLPL PDSCCQACKD EASEQSDEED SVQSLHGVRH PQDPCSSDAG

                    301                                                 350
     chordin_ed7    RKRGPGTPAP TGLSAPLSFI PRHFRPKGAG STTVKIVLKE KHXKACVHGG
chordin_ed6TR_2     RKRGPGTPAP TGLSAPLSFI PRHFRPKGAG STTVKIVLKE KHXKACVHGG
chordin_ed6TR_1     RKRGPGTPAP TGLSAPLSFI PRHFRPKGAG STTVKIVLKE KHXKACVHGG

                    351                                                 400
     chordin_ed7    KTYSHGEVWH PAFRAFGPCP CILCTCEDGR QDCQRVTCPT KYPCRHPEKV
chordin_ed6TR_2     KTYSHGEVWH PAFRAFGPCP CILCTCEDGR QDCQRVTCPT KYPCRHPEKV
chordin_ed6TR_1     KTYSHGEVWH PAFRAFGPCP CILCTCEDGR QDCQRVTCPT KYPCRHPEKV
```

FIG. 5 (CONT.[1])

```
                401                                                 450
    chordin_ed7 AGKCCKICPE DKADPGHSEI SSTRCPKAPG RVLVHTSVSP SPDNLRRFAL
chordin_ed6TR_2 AGKCCKICPE DKADPGHSEI SSTRCPKAPG RVLVHTSVSP SPDNLRRFAL
chordin_ed6TR_1 AGKCCKICPE DKADPGHSEI SSTRCPKAPG RVLVHTSVSP SPDNLRRFAL

                451                                                 500
    chordin_ed7 EHEASDLVEI YLWKLVKDEE TEAQRGEVPG PRPHSQNFHL TQIKKVRKQD
chordin_ed6TR_2 EHEASDLVEI YLWKLVKDEE TEAQRGEVPG PRPHSQNFHL TQIKKVRKQD
chordin_ed6TR_1 EHEASDLVEI YLWKLVKDEE TEAQRGEVPG PRPHSQNFHL TQIKKVRKQD

                501                                                 542
    chordin_ed7 FQKEAQHFRL LAGPHEGHWN VFLAQTLELK VTASPDKVTK T*
chordin_ed6TR_2 FQKEAQHFRL LAGPHEGHWN VFLAQTLELK VTASPDKVTK T*
chordin_ed6TR_1 FQKEAQHFRL LAGPHEGHWN VFLAQTLELK VTASPDKVTK T*
```

FIG. 5 (CONT.[2])

```
862 TCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGG 911
    |||   |||      ::::::          |||      :::   :::||
  3 SerTyrHisArgSerHisTyrAspProProProSerArgGlnAlaGlyGl 19

912 GAGAAAGAGAGGCCCGGGCACCCCAGCCCCCACTGGCCTCAGCGCCCCTC 961
          |   :::|||   ||||||:::   :::      |||
 19 yLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeuMetAsp. 35

962 TGAGCTTCATCCCTCGCCACTTCATACCCAAGGGAGCAGGCAGCACAACT 1011
                    :::   |||:::::::|||
  36 ..........................SerGlnGlnAlaSerGlyThrIle 43

1012 GTCAAGATCGTCCTGAAGGAGAAACATAAG......AAAGCCTGTGTGCA 1055
      |||:::|||||||:::::::::|||||||||      ::::::||||||
  44 ValGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysValSe 60

1056 TGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTG 1105
      :::|||||||||||||||||||||||| .|||||||||   :::||||
  60 rAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuArgA 77
```

FIG. 6

```
1106 CCTTCGGCCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAG 1155
     ||||||||   :::   |||:::||||||||||||||:::      :::|||
  77 laPheGlyIleValGluCysValLeuCysThrCysAsnValThrLysGln 93

1156 GACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTCACCCCGA 1205
     :::|||:::::::::   ||||||::::::||||||||::::::|||::
  94 GluCysLysLysIleHisCysProAsnArgTyrProCysLysTyrProGl 110

1206 GAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAAGCAGAC. 1254
       :|||:::   ||||||||||||||::::||||||      ||||||
 110 nLysIleAspGlyLysCysCysLysValCysProGlyLysLysAlaLysG 127

1255 .........CCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCCAAG 1293
         ||||||::::|||   :::   ::::::      |||   :::
 127 luGluLeuProGlyGlnSerPheAspAsnLysGlyTyrPheCysGlyGlu 143

1294 GCACCGGGCCGGGTCCTCGTCCACACATCGGTA...TCCCCAAGCCCAGA 1340
           :::   |||:::   ||||||   .      :::   ::
 144 Glu......ThrMetProValTyrGluSerValPheMetGluAspGlyGl 158
```

FIG. 6 (CONT.[1])

```
1341 CAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTCGGACCTGGTGGAGA 1390
     ::::   |||:::::::|||||||||   |||              ||||||:
 158 uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175

1391 TCTACCTCTGGAAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNNNNN 1440
                        ::::::::|||   :::
 175 alHisValTrpThrIle..............................  180

1441 NNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGAATCTTCCACTTGACTCAGA 1490
                     |||::: ||||||         |
 181 ............ArgLysGlyIleLeuGlnHis.PheHis.........I 190

1491 TCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGA 1540
     ||:::|||:::   |||:::   |||:::   |||       ||||||:::
 190 leGluLysIleSerLysArgMetPheGlu...GluLeuProHisPheLys 205

1541 CTGCTCGCTGGCCCCCACGAAGGTCACTGGAACGTCTTCCTAGCCCAGAC 1590
          |||::::::                 :::::|||:::::::|||
 206 LeuValThrArgThrThrLeuSerGlnTrpLysIlePheThrGluGlyGl 222
```

FIG. 6 (CONT.[2])

```
1591 CCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAAC 1640
       :::::::::      :::|||                        +++
 222 uAlaGlnIleSerGlnMetCysSer.......................... 230

1641 AAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGCTGTTATTATATA 1690
        :::   ||||||  ||||||   :::                :::
 231 .....SerArgValCysArgThrGluLeuGluAspLeuValLysValLeu 245

                1691 TTAATAAATAAGAAGTTGCATAACCAT 1717
          ::::::::::      :::|||
246 TyrLeuGluArgSerGluLysGlyHis 254
```

FIG. 6 (CONT.[3])

```
  3 CTTCCCCCTTTCTTTGATCGCCTCTCC.............CTTCTGCTGGA 40
    |||||||||      ::::::   :::              |||   |||||
390 LeuProProValLysSerGlnAlaAlaGlyHisAlaTrpLeuSerLeuAs 406

 41 CCTTCCTTCGTCTCTCCATCTCTCCCTCCTT..................... 71
              |             ||||||   :::::::||
406 pThrHisCysHisLeuHisTyrGluValLeuLeuAlaGlyLeuGlyGlyS 423

 72 ..TCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCC 119
      :::      ::::::::::::   |||:::   ||||||+++|||
423 erGluGlnGlyThrValThrAlaHisLeuLeuGlyProProGlyThr... 438

120 CTTCCTGCCCTCCTTTCCTGCCCACCGCTGCTTCCTGGCCCTTCTCCGAC 169
                          |||:::|||
439 ..................................ProGlyProAr 442

170 CCCGCTCTAGCAG.............CAGACCTCCTGGGGTCTGTGGGTTG 207
      |||+++:::              :::   :::   |||:::       |
442 gArgLeuLeuLysGlyPheTyrGlySerGluAlaGlnGlyValValLysA 459
```

FIG. 7

```
208 ATCTGTGGCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGAC 257
              |||||   |||      ||||||   |||
459 spLeuGluProGluLeuLeuArgHisLeu..................... 468

258 TCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCC...CG 304
     |||   |||   |||:::+++                  ||||||   ||
469 ...AlaLysGlyMetAlaSerLeuLeuIleThrThrLysGlySerProAr 484

305 AGGTGAG.....................................GGTC 315
    |||||||                                     |||
484 gGlyGluLeuArgGlyGlnValHisIleAlaAsnGlnCysGluValGlyG 501

316 CTCTCCTCCTT..............GCTGGGACTCGCGCT..... 341
          |||   |||                 |||:::||||||
501 lyLeuArgLeuGluAlaAlaGlyAlaGluGlyValArgAlaLeuGlyAla 517

342 .....................................GCTCT 346
                             |||||
518 ProAspProAlaSerAlaAlaProProValValProGlyLeuProAlaLe 534
```

FIG. 7 (CONT.[1])

```
347 GGTTCCC......CCTGGACTCCCACGCTCGAGCCCGCCCAGACATGTTC 390
          |:::|||      ||||||   ||| :::|||   |||
534 uAlaProAlaLysProGlyGlyPro.GlyArgProArgAspProAsnThr 550

391 TGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTA 440
     |||:::|||:::|||::::::          |||     |||   |||
551 CysPhePheGluGlyGlnGlnArgProHisGlyAlaArgTrpAlaProAs 567

441 CTTGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGG 490
      :::|||                 |||     |||||||||:::::
567 nTyrAspPro.............LeuCysSerLeuCysThrCysGlnArgA 580

491 GCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCC 540
     :::   |||   |||      :::   |||||||||      ||||||
580 rgThr...ValIleCysAspProValValCysProProProSerCysPro 595

541 CAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAA..... 585
      :::||||||      |||:::|||||||||||||   |||   |||
596 HisProValGlnAlaProAspGlnCysCysProValCysProGluLysGl 612
```

FIG. 7 (CONT.^{2})

```
586 ..................CCTCACACTCCCTCTGGACTCCGGGCCCCACCAA 619
                  |||       |||   :::   |||   |||   :
612 nAspValArgAspLeuProGlyLeuProArgSer...ArgAspProGlyG 628

620 AGTCCTGCCAGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGT 669
          :::::|||      :::|||                 ::::::
628 luGlyCysTyrPheAspGlyAspArgSerTrpArgAlaAlaGlyThrArg 644

670 GCCCATGAGCTGTTCCCCTCCCGCCTGCCCAACCAGTGTGTCCTCTGCAG 719
      |||   :::   |||                 :::|||::::::|||::
645 TrpHisProValValProProPheGlyLeuIleLysCysAlaValCysTh 661

720 CTGCACA......GAGGGCCAGATCTACTGCGGGCTCACAACCTGCCCCG 763
    :|||          |||::::::::::|||    :::   ||||||:
661 rCysLysGlyGlyThrGlyGluValHisCysGluLysValGlnCysProA 678

764 AACCAGGCTGCCCAGCACCCCTCCCGCTG...CCAGACTCCTGCTGCCAG 810
    ::   :::|||     |||:::   ::: . |||   :::|||||::::
678 rgLeuAlaCysAlaGlnProValArgValAsnProThrAspCysCysLys 694
```

FIG. 7 (CONT.[3])

```
811 GCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACCGTGTGCA 860
                           |||
695 GlnCys..................................... 696

861 GTCGCTCCATGGGGTGAGACATCCTCAG......GATCCATGTTCCAGTG 904
      :::   :::      |||||||||       ||||||   ::::::|
697 .ProValGlySerGlyAlaHisProGlnLeuGlyAspProMetGlnAlaA 713

905 ATGCTGGGAGAAAGAGAGGCCCGGGCACCCCAGCCCCCACTGGCCTCAGC 954
                 ||                  ||||||
713 sp.............GlyPro..................... 715

955 GCCCCTCTGAGCTTCATCCCTCGCCACTTCATACCCAAGGGAGCAGGCAG 1004

715 ..................................................... 715

1005 CACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGC 1054
                          ::::::|||
716 ..............................ArgGlyCysArgP 720
```

FIG. 7 (CONT.[4])

```
1055 ATGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGT 1104
        :::|||:::   :::   :::::::::   |||||||||:::
 720 heAlaGlyGlnTrpPheProGluSerGlnSerTrpHisProSerValPro 736

1105 GCCTTCGGCCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCA 1154
        ||||||   :::   ||||||   |||   |||      |||
 737 ProPheGlyGluMetSerCysIleThrCysArgCysGlyAlaGlyValPr 753

1155 GGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTCACCCCG 1204
       |||:::|||      |||                |||         :
 753 oHisCysGluArgAspAspCysSerLeuProLeuSerCysGlySerGlyL 770

1205 AGAAAGTGGCTGGGAAGTGCTGCAAGATTTGC..................  1236
             :::::     ::::::||||||:::   |||
 770 ysGlu......SerArgCysCysSerArgCysThrAlaHisArgArgPro 784

1237 ...CCAGAGGACAAAGCAGACCCT 1257
        ||||||   ::::::||||||
 785 AlaProGluThrArgThrAspPro 792
```

FIG. 7 (CONT.[5])

```
  3 CTTCCCCCTTTCTTTGATCGCCTCTCC.............CTTCTGCTGGA 40
    |||||||||      ::::::   :::              |||   |||||
540 LeuProProValArgSerGlnAlaAlaGlyHisAlaTrpLeuSerLeuAs 556

 41 CCTTCCTTCGTCTCTCCATCTCTCCCTCCTT...................T 72
    |             ||||||   :::::::||                    |
556 pThrHisCysHisLeuHisTyrGluValLeuLeuAlaGlyLeuGlyGlyS 573

 73 CCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTT 122
        ||   ::::::      |||                  +++
573 erGluGlnGlyThrValThr.............................. 579

123 CCTGCCCTCCTTTCCTGCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCC 172
          |||   |||      ||||||   :::||||||||||
580 ...AlaHisLeuLeuGlyProProGlyMetProGlyPro.......... 591

173 GCTCTAGCAGCAG.........................ACCTCCTGGGGTC 198
     +++|||:::                            :::   |||:
592 .......GlnArgLeuLeuLysGlyPheTyrGlySerGluAlaGlnGlyV 606
```

FIG. 8

```
199 TGTGGGTTGATCTGTGGCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTT 248
          ::      ||||||   |||:::   ||||||   |||
606 alValLysAspLeuGluProValLeuLeuArgHisLeu..... 618

249 CCTCCCGACTCCGCTCCCGGACCAGCGGCC..... 278
                    |||   |||   |||:::
619 ............AlaGlnGlyThrAlaSerLeuLeuIleThrThrLysSe 631

278 ..... 278

631 rSerProArgGlyGluLeuArgGlyGlnValHisIleAlaSerGlnCysG 648

279 .....TGACCCTGGGGA 290
                      +++|||   :::
648 luAlaGlyGlyLeuArgLeuAlaSerGluGlyValGlnMetProLeuAla 664

291 AAGGATGGTTCCCGAGGTGAGGGTCCTCTCCTCCTTGCTGGGACT...CG 337
          :::|||:::   :::   :::|||:::|||   ||||||
665 ProAsnGlyGluAlaAlaThrSerProMetLeuProAlaGlyProGlyPr 681
```

FIG. 8 (CONT.[1])

```
338 CGCTGCTCTGGTTCCCCCT......GGACTCCCACGCTCGAGCCCGCCCA 381
       |||   ||||||           |||   ||| :::|||   |||
681 oGluAlaProValProAlaLysHisGlySerPro.GlyArgProArgAsp 697

382 GACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTG 431
     |||:::|||:::|||:::::          |||      ||
698 ProAsnThrCysPhePheGluGlyGlnGlnArgProHisGlyAlaArgTr 714

432 GCACCCCTACTTGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCT 481
    |   |||      :::|||                |||      |||   |
714 pAlaProAsnTyrAspPro.............LeuCysSerLeuCysIleC 727

482 GCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTC 531
     ||:::::::   :::   |||   |||      :::   |||||||||
727 ysGlnArgArgThr...ValIleCysAspProValValCysProProPro 742

532 CACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGT 581
      ||||||:::||||||          :::|||||||||||||   |||
743 SerCysProHisProValGlnAlaLeuAspGlnCysCysProValCysPr 759
```

FIG. 8 (CONT.[2])

```
582 GGAA.....CCTCACACTCCCTCTGGACTCCGGG 610
        |||          |||     |||:::
759 oGluLysGlnArgSerArgAspLeuProSerLeuProAsn......LeuG 774

611 CCCCACCAAAGTCCTGCCAGCACAACGGGACCATGTACCAACACGGAGAG 660
      |||   ::::::|||      :::|||            ::::::
774 luProGlyGluGlyCysTyrPheAspGlyAspArgSerTrpArgAlaAla 790

661 ATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCTGCCCAACCAGTGTGT 710
        |||   :::   |||                 :::|||::
791 GlyThrArgTrpHisProValValProProPheGlyLeuIleLysCysAl 807

711 CCTCTGCAGCTGC......ACAGAGGGCCAGATCTACTGCGGGCTCACAA 754
    ::::|||:::|||      :::   |||::::::::::|||     :::
807 aValCysThrCysLysGlyAlaThrGlyGluValHisCysGluLysValG 824

755 CCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCGCTG...CCAGACTCC 801
     ||||||:::   :::|||      |||:::          |||   :::
824 lnCysProArgLeuAlaCysAlaGlnProValArgAlaAsnProThrAsp 840
```

FIG. 8 (CONT.[3])

```
802 TGCTGCCAGGCCTGTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGA 851
    ||||||||:::  |||                                   
841 CysCysLysGlnCys.....................................845
                                                        
852 CCGTGTGCAGTCGGTGGGTGAGACATCCTCAGGATCCATGTTCCATGGGA 901
    |||   :::|                                         
846 .....ProValGlyS.....................................849
                                                        
902 GTGATGCTGGGAGAAAGAGGCCCGGGCACCCCCAGCCCCCACTGGCCTC 951
    ||    |||  ||||  |||                               
849 erGlyThrAsnAlaLysLeuGlyAsp.....ProMetGlnAla.....861
                                                        
952 AGCGCCCCCTCTGAGAGCTTCATCCCTCGCCACTTCATACCCAAGGGAGC 1001
    ::::::|||                                          
862 AspGlyPro.....................................GCAGG 1001
                                                        
1002 CAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTG 1051
     :::::|||                                          
865 .....ArgGlyCysA.....................................868
```

FIG. 8 (CONT.[4])

```
1052 TGCATGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTC 1101
         :::|||:::   :::   :::::::::   |||||||||:::
 868 rgPheAlaGlyGlnTrpPheProGluAsnGlnSerTrpHisProSerVal 884

1102 CGTGCCTTCGGCCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCG 1151
         ||||||   :::   ||||||   |||   |||       |||
 885 ProProPheGlyGluMetSerCysIleThrCysArgCysGlyAlaGlyVa 901

1152 CCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTCACC 1201
            |||:::|||      |||                  |||
 901 lProHisCysGluArgAspAspCysSerProProLeuSerCysGlySerG 918

1202 CCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGC..............  1236
             ::::::     ::::::||||||:::   |||
 918 lyLysGlu......SerArgCysCysSerHisCysThrAlaGlnArgSer 932

 1237 ..................CCAGAGGACAAAGCAGACCCTGGCCACAGT 1266
                  ||||||   :::   :::      ||||||
  933 SerGluThrArgThrLeuProGluLeuGluLysGluAlaGluHisSer 948
```

FIG. 8 (CONT.[5])

```
862 TCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGG 911
    |||   |||      ::::::          |||      :::   :::||
  3 SerTyrHisArgSerHisTyrAspProProProSerArgGlnAlaGlyGl 19

912 GAGAAAGAGAGGCCCGGGCACCCCAGCCCCCACTGGCCTCAGCGCCCCTC 961
          |   :::|||   |||||||:::   :::      |||
 19 yLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeu..... 33

962 TGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACT 1011
                :::      :::   |||::::::|||
 34 .....MetAspSerGlnGlnAlaSerGlyThrIle 43

1012 GTCAAGATCGTCCTGAAGGAGAAACATAAG......AAAGCCTGTGTGCA 1055
      |||:::||||||:::::::::|||||||||      ::::::||||||
  44 ValGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysValSe 60

1056 TGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTG 1105
     :::|||||||||||||||||||||||   |||||||||   :::||||
  60 rAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuArgA 77
```

FIG. 9

```
1106 CCTTCGGCCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAG 1155
     ||||||||   :::   |||:::|||||||||||||:::      :::|||
  77 laPheGlyIleValGluCysValLeuCysThrCysAsnValThrLysGln 93

1156 GACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTCACCCCGA 1205
     :::|||:::::::::   ||||||:::::||||||||:::::|||::
  94 GluCysLysLysIleHisCysProAsnArgTyrProCysLysTyrProGl 110

1206 GAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAAGCAGAC. 1254
       :|||:::   |||||||||||||||:::||||||      ||||||
 110 nLysIleAspGlyLysCysCysLysValCysProGlyLysLysAlaLysG 127

1255 .........CCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCCAAG 1293
         ||||||:::|||   :::   ::::::      |||   :::
 127 luGluLeuProGlyGlnSerPheAspAsnLysGlyTyrPheCysGlyGlu 143

1294 GCACCGGGCCGGGTCCTCGTCCACACATCGGTA...TCCCCAAGCCCAGA 1340
           :::   |||:::   ||||||          :::   ::
 144 Glu......ThrMetProValTyrGluSerValPheMetGluAspGlyGl 158
```

FIG. 9 (CONT.[1])

```
1341 CAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTCGGACTTGGTGGAGA 1390
     ::::   |||::::::|||||||||   |||              ||||||:
 158 uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175

1391 TCTACCTCTGGAAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNNNN 1440
                      :::::::::|||   :::
 175 alHisValTrpThrIle..............................  180

1441 NNNNNNNNNNNNNNNNNNNNNNNNNNNNCAGAATCTTCCACTTGACTCAGA 1490
                     |||::: ||||||         |
 181 ............ArgLysGlyIleLeuGlnHis.PheHis.........I 190

1491 TCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGA 1540
     ||:::|||:::   |||:::   |||:::   |||      ||||||:::
 190 leGluLysIleSerLysArgMetPheGlu...GluLeuProHisPheLys 205

1541 CTGCTCGCTGGCCCCCACGAAGGTCACTGGAACGTCTTCCTAGCCCAGAC 1590
          |||::::::              ::::::|||::::::|||
 206 LeuValThrArgThrThrLeuSerGlnTrpLysIlePheThrGluGlyGl 222
```

FIG. 9 (CONT.[2])

PCT/IL00/00736

09/890456

```
1591 CCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAAC 1640
       :::::::::      :::|||                          +++
 222 uAlaGlnIleSerGlnMetCysSer.......................... 230

1641 AAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATA 1690
        :::   ||||||   ||||||   :::                :::
 231 .....SerArgValCysArgThrGluLeuGluAspLeuValLysValLeu 245

          1691 TTAATAAATAAGAAGTTGCATAACCAT 1717
               ::::::::::::      :::|||
          246 TyrLeuGluArgSerGluLysGlyHis 254
```

FIG. 9 (CONT.[3])

```
  3 CTTCCCCCTTTCTTTGATCGCCTCTCC.............CTTCTGCTGGA 40
    |||||||||      ::::::   :::              |||   |||||
390 LeuProProValLysSerGlnAlaAlaGlyHisAlaTrpLeuSerLeuAs 406

 41 CCTTCCTTCGTCTCTCCATCTCTCCCTCCTT..................... 71
               |              ||||||   :::::::|||
406 pThrHisCysHisLeuHisTyrGluValLeuLeuAlaGlyLeuGlyGlyS 423

 72 ..TCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCC 119
      :::      ::::::::::::   |||:::   ||||||++++|||
423 erGluGlnGlyThrValThrAlaHisLeuLeuGlyProProGlyThr... 438

120 CTTCCTGCCCTCCTTTCCTGCCCACCGCTGCTTCCTGGCCCTTCTCCGAC 169
                           |||:::|||
439 ..................................ProGlyProAr 442

170 CCCGCTCTAGCAG.............CAGACCTCCTGGGGTCTGTGGGTTG 207
      |||+++:::                :::   :::   |||:::      |
442 gArgLeuLeuLysGlyPheTyrGlySerGluAlaGlnGlyValValLysA 459
```

FIG. 10

```
208 ATCTGTGGCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGAC 257
              |||||   |||     ||||||   |||
459 spLeuGluProGluLeuLeuArgHisLeu..................... 468

258 TCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCC...CG 304
     |||   |||   |||:::+++                  ||||||   ||
469 ...AlaLysGlyMetAlaSerLeuLeuIleThrThrLysGlySerProAr 484

305 AGGTGAG.....................................GGTC 315
    |||||||                                     |||
484 gGlyGluLeuArgGlyGlnValHisIleAlaAsnGlnCysGluValGlyG 501

316 CTCTCCTCCTT..............GCTGGGACTCGCGCT......... 341
          |||   |||                 |||:::||||||
501 lyLeuArgLeuGluAlaAlaGlyAlaGluGlyValArgAlaLeuGlyAla 517

342 ....................................GCTCT 346
                                  |||||
518 ProAspProAlaSerAlaAlaProProValValProGlyLeuProAlaLe 534
```

FIG. 10 (CONT.[1])

```
347 GGTTCCC......CCTGGACTCCCACGCTCGAGCCCGCCCAGACATGTTC 390
          |:::|||      ||||||   ||| :::|||   |||
534 uAlaProAlaLysProGlyGlyPro.GlyArgProArgAspProAsnThr 550

391 TGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTA 440
     |||:::|||:::|||:::::          |||     |||   |||
551 CysPhePheGluGlyGlnGlnArgProHisGlyAlaArgTrpAlaProAs 567

441 CTTGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGG 490
      :::|||              |||      |||||||||:::::
567 nTyrAspPro.............LeuCysSerLeuCysThrCysGlnArgA 580

491 GCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCC 540
     :::   |||   |||      :::   |||||||||      ||||||
580 rgThr...ValIleCysAspProValValCysProProProSerCysPro 595

541 CAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAA..... 585
      :::||||||      |||:::|||||||||||||   |||   |||
596 HisProValGlnAlaProAspGlnCysCysProValCysProGluLysGl 612
```

FIG. 10 (CONT.[2])

```
586 ..................CCTCACACTCCCTCTGGACTCCGGGCCCCACCAA 619
            |||       |||    :::    |||    |||    :
612 nAspValArgAspLeuProGlyLeuProArgSer...ArgAspProGlyG 628

620 AGTCCTGCCAGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGT 669
       :::::|||       :::|||                :::::
628 luGlyCysTyrPheAspGlyAspArgSerTrpArgAlaAlaGlyThrArg 644

670 GCCCATGAGCTGTTCCCCTCCCGCCTGCCCAACCAGTGTGTCCTCTGCAG 719
     |||    :::    |||                    :::|||::::::|||::
645 TrpHisProValValProProPheGlyLeuIleLysCysAlaValCysTh 661

720 CTGCACA......GAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCG 763
    :|||             |||::::::::::|||      :::    ||||||:
661 rCysLysGlyGlyThrGlyGluValHisCysGluLysValGlnCysProA 678

764 AACCAGGCTGCCCAGCACCCCTCCCGCTG...CCAGACTCCTGCTGCCAG 810
    ::    :::|||       |||:::    :::    |||    :::||||||:::
678 rgLeuAlaCysAlaGlnProValArgValAsnProThrAspCysCysLys 694
```

FIG. 10 (CONT.[3])

```
811 GCCTGCAAA...GGTGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGT 857
                  |||      |||::::::::::
695 GlnCysProValGlySerGlyAla.......................... 702

858 GCAGTCGCTCCATGGGGTGAGACATCCTCAG......GATCCATGTTCCA 901
              ||||||||      ||||||   ::::
703 ......................HisProGlnLeuGlyAspProMetGlnA 712

902 GTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCCAGCCCCCACTGGCCTC 951
                 ::|||                 ||||||
712 laAsp..............GlyPro.......................... 715

952 AGCGCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGG 1001

715 ..................................................... 715

1002 CAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTG 1051
                          ::::::|||
716 ...................................ArgGlyCysA 719
```

FIG. 10 (CONT.[4])

```
1052 TGCATGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTC 1101
         :::|||:::   :::   :::::::::   |||||||||:::
 719 rgPheAlaGlyGlnTrpPheProGluSerGlnSerTrpHisProSerVal 735

1102 CGTGCCTTCGGCCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCG 1151
         ||||||   :::   ||||||   |||   |||       |||
 736 ProProPheGlyGluMetSerCysIleThrCysArgCysGlyAlaGlyVa 752

1152 CCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTCACC 1201
           |||:::|||      |||                  |||
 752 lProHisCysGluArgAspAspCysSerLeuProLeuSerCysGlySerG 769

1202 CCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGC..............  1236
             ::::::      ::::::||||||:::   |||
 769 lyLysGlu......SerArgCysCysSerArgCysThrAlaHisArgArg 783

1237 ......CCAGAGGACAAAGCAGACCCT 1257
           ||||||   ::::::||||||
 784 ProAlaProGluThrArgThrAspPro 792
```

FIG. 10 (CONT.[5])

```
655 TCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGG 704
    |||   |||      ::::::          |||      :::   :::||
  3 SerTyrHisArgSerHisTyrAspProProProSerArgGlnAlaGlyGl 19

705 GAGAAAGAGAGGCCCGGGCACCCCAGCCCCCACTGGCCTCAGCGCCCCTC 754
          |   :::|||   ||||||:::   :::      |||
 19 yLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeu..... 33

755 TGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACT 804
                :::      :::   |||::::::|||
 34 .....MetAspSerGlnGlnAlaSerGlyThrIle 43

805 GTCAAGATCGTCCTGAAGGAGAAACATAAG......AAAGCCTGTGTGCA 848
     |||:::||||||:::::::::|||||||||      ::::::||||||
 44 ValGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysValSe 60

849 TGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTG 898
    :::||||||||||||||||||||||||   ||||||||   :::||||
 60 rAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuArgA 77
```

FIG. 11

```
899 CCTTCGGCCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAG 948
    ||||||||   :::   |||:::|||||||||||||:::      :::|||
 77 laPheGlyIleValGluCysValLeuCysThrCysAsnValThrLysGln 93

949 GACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTCACCCCGA 998
    :::|||:::::::::   ||||||:::::||||||||||:::::|||::
 94 GluCysLysLysIleHisCysProAsnArgTyrProCysLysTyrProGl 110

999 GAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAAGCAGAC. 1047
      :|||:::   ||||||||||||||::||||||      ||||||
110 nLysIleAspGlyLysCysCysLysValCysProGlyLysLysAlaLysG 127

1048 .........CCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCCAAG 1086
        ||||||:::|||   :::   ::::::      |||   :::
127 luGluLeuProGlyGlnSerPheAspAsnLysGlyTyrPheCysGlyGlu 143

1087 GCACCGGGCCGGGTCCTCGTCCACACATCGGTA...TCCCCAAGCCCAGA 1133
          :::   |||:::   ||||||          :::   ::
144 Glu......ThrMetProValTyrGluSerValPheMetGluAspGlyGl 158
```

FIG. 11 (CONT.[1])

```
1134 CAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTCGGACTTGGTGGAGA 1183
     ::::   |||::::::|||||||||   |||              ||||||:
 158 uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175

1184 TCTACCTCTGGAAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNNNNN 1233
                     ::::::::|||   :::
 175 alHisValTrpThrIle..............................  180

1234 NNNNNNNNNNNNNNNNNNNNNNNNNNNCAGAATTTCCACTTGACTCAGAT 1283
                    |||:::||||||         ||
 181 ............ArgLysGlyIleLeuGlnHisPheHis.........Il 190

1284 CAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGAC 1333
     |:::|||:::   |||:::   |||:::   |||       ||||||:::|
 190 eGluLysIleSerLysArgMetPheGlu...GluLeuProHisPheLysL 206
```

FIG. 11 (CONT.[2])

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```
1334 TGCTCGCTGGCCCCCACGAAGGTCACTGGAACGTCTTCCTAGCCCAGACC 1383
           ||::::::               ::::::|||::::::|||
 206 euValThrArgThrThrLeuSerGlnTrpLysIlePheThrGluGlyGlu 222

1384 CTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACA 1433
        :::::::::     :::|||                     +++
 223 AlaGlnIleSerGlnMetCysSer.......................... 230

1434 AAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATAT 1483
          :::   ||||||   ||||||   :::               :::
 231 ....SerArgValCysArgThrGluLeuGluAspLeuValLysValLeuT 246

            1484 TAATAAATAAGAAGTTGCATAACCAT 1509
                   ::::::::::::     :::|||
             246 yrLeuGluArgSerGluLysGlyHis 254
```

FIG. 11 (CONT.[3])

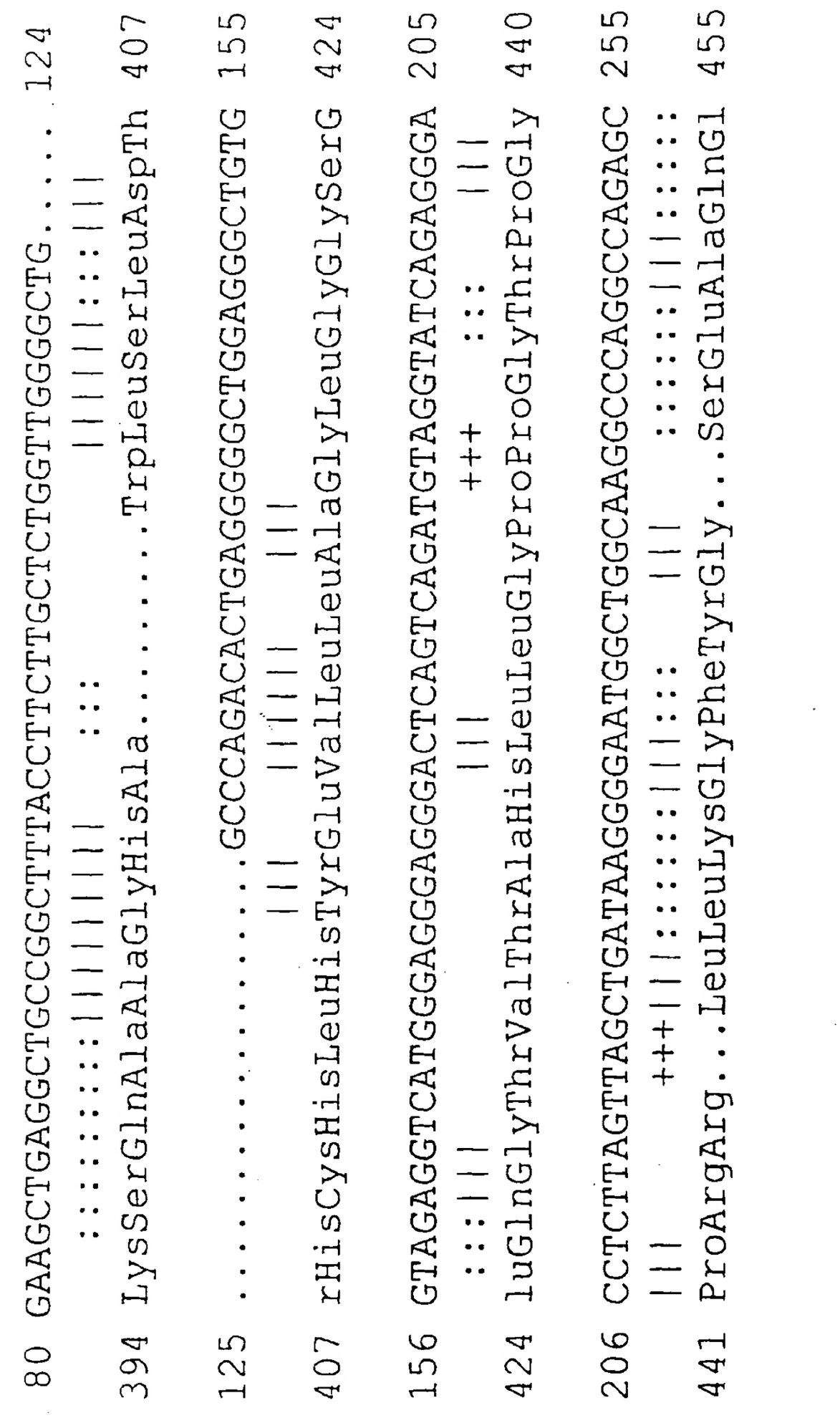
80 GAAGCTGAGGCTGCCGGCTTTACCTTCTTGCTCTGGTTGGGGCTG...
394 LysSerGlnAlaAlaGlyHisAla.....TrpLeuSerLeuAs
125 .....GCCCAGACACTGAGGGGCTGGAGGGCT
407 rHisCysHisLeuHisTyrGluValLeuAlaGlyLeuGlyGlyS
156 GTAGAGGTCATGGGAGGGAGGGACTCAGTCAGATGTAGGTATCAGAG
424 luGlnGlyThrValThrAlaHisLeuGlyProProGlyThrPro
206 CCTCTTAGTTAGCTGATAAGGGGAATGGCTGGCAAGGCCCAGGCCAG
441 ProArgArg...LeuLeuLysGlyPheTyrGly...SerGluAlaGl

FIG. 12

```
256 TTGGTTTAAATATCAAGCTGGGGTCAAATGCAAAATCATCAGAAAAGTGG 305
    :      |||              ::::::   ::::::::::|||   :::|
455 yValValLys.........AspLeuGluProGluLeuLeuArgHisLeuA 469

306 CC..............TTGTTAATTTCAGCAAAG.............. 325
            ||                |||||||||::::::|||
469 laLysGlyMetAlaSerLeuLeuIleThrThrLysGlySerProArgGly 485

326 ..............ATTCACATG..........................  334
                          :::|||:::
486 GluLeuArgGlyGlnValHisIleAlaAsnGlnCysGluValGlyGlyLe 502

335 .....................................A 335

502 uArgLeuGluAlaAlaGlyAlaGluGlyValArgAlaLeuGlyAlaProA 519

336 AACCTCATTTTCTTCTTCCTCCTGCCCCTCCC......CCACTGCA.GAA 378
          |||              ||||||:::   |||      |||
519 spProAlaSerAlaAlaProProValValProGlyLeuProAlaLeuAla 535
```

FIG. 12 (CONT.[1])

```
379 CCTCACACTCCCTCTGGACTCCGGGCCCCA......CCAAAGTCCTGCCA 422
     |||      |||:::|||          |||      |||::::::|||
536 ProAlaLysProGlyGlyProGlyArgProArgAspProAsnThrCysPh 552

423 GCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGC 472
          :::|||   :::      ||||||      ::::::
552 ePheGluGlyGlnGlnArgProHisGlyAlaArgTrpAla..... 565

473 TGTTCCCCTCCCGCCTGCCCAACCAG.........TGTGTCCTCTGCAGC 513
           ||||||             |||   ||||||:::
566 ..................ProAsnTyrAspProLeuCysSerLeuCysThr 576

514 TGCACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAGG 563
    |||   :::      :::   |||      ::::::||||||   |||::
577 CysGlnArgArgThrValIleCysAspProValValCysProProProSe 593

564 CTGCCCAGCACCCCTCCCGCTGCCAGACTCCTGCTGCCAGGCCTGCAAAG 613
      :||||||   |||:::      ||||||:::||||||   :::|||
593 rCysProHisProValGlnAlaProAspGlnCysCysProValCys.... 608
```

FIG. 12 (CONT.^{2})

```
614 ATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCAT 663
                 |||::::::::::|||::::::|||
609 ....................ProGluLysGlnAspValArgAspLeuPro 618

664 GGGGTGAGACATCCTCAGGATCCA.........TGTTCCAGTGATGCTGG 704
     |||:::   :::   :::||||||          |||      |||:::
619 GlyLeuProArgSerArgAspProGlyGluGlyCysTyrPheAspGlyAs 635

705 GAGAAAG...AGAGGCCCGGGCACC..............CCAGCCCCCA 736
     |||:::   |||:::   ||||||                  |||
635 pArgSerTrpArgAlaAlaGlyThrArgTrpHisProValValProProP 652

737 CTGGCCTC..................................... 744
                          ||||||
652 heGlyLeuIleLysCysAlaValCysThrCysLysGlyGlyThrGlyGlu 668

745 ..................................AGCGCCCCTCT 755
                         :::   |||::
669 ValHisCysGluLysValGlnCysProArgLeuAlaCysAlaGlnProVa 685
```

FIG. 12 (CONT.[3])

```
756 GAGCTTCATCCCTCGCCACTTC.........AGACCCAAGGGAGCAGGCA 796
    :         |||                       |||   |||:::|||:
685 lArgValAsnProThrAspCysCysLysGlnCysProValGlySerGlyA 702

797 GC...ACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGT 843
    ::         :::         ::::::                :::::::||
702 laHisProGlnLeuGlyAspProMetGlnAlaAspGlyProArgGlyCys 718

844 GTGCATGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTT 893
        :::|||:::   :::   :::::::::   |||||||||:::
719 ArgPheAlaGlyGlnTrpPheProGluSerGlnSerTrpHisProSerVa 735

894 CCGTGCCTTCGGCCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCC 943
        ||||||   :::   ||||||   |||   |||       |||
735 lProProPheGlyGluMetSerCysIleThrCysArgCysGlyAlaGlyV 752

944 GCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTCAC 993
          |||:::|||      |||                  |||
752 alProHisCysGluArgAspAspCysSerLeuProLeuSerCysGlySer 768
```

FIG. 12 (CONT.[4])

```
994 CCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGC..............  1029
              ::::::      ::::::||||||:::   |||
769 GlyLysGlu.....SerArgCysCysSerArgCysThrAlaHisArgAr  783

          1030 .......CCAGAGGACAAAGCAGACCCT 1050
                     ||||||   ::::::||||||
           783 gProAlaProGluThrArgThrAspPro 792
```

FIG. 12 (CONT.[5])

```
486 TGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTA 535
    |||:::|||:::|||:::::::::::::   |||:::::::|||   |||
691 CysPhePheGluGlyGluGlnHisThrHisGlySerGlnTrpThrProGl 707

536 CTTGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGG 585
      :::                    |||:::   |||||||||:::::
707 nTyrAsnThr..............CysPheThrCysThrCysGlnLysL 719

586 GCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCC 635
      :::   |||   |||       :::   ||||||   :::   |||
719 ysThr...ValIleCysAspProValMetCysProThrLeuSerCysThr 734

636 CAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCA 685
      :::   |||         :::||||||||||||||   |||   |||
735 HisThrValGlnProGluAspGlnCysCysProIleCysGluGluLysLy 751

686 CACTCCCTCTGGACTCCGGGCC.....................CCACCAAAGT 717
      :::         |||                          |||::::
751 sGluSerLysGluThrAlaAlaValGluLysValGluGluAsnProGluG 768
```

FIG. 13

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```
718 CCTGCCAGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCC 767
      ::|||      :::|||   :::   :::|||:::          :::
768 lyCysTyrPheGluGlyAspGlnLysMetHisAlaProGlyThrThrTrp 784

768 CATGAGCTGTTCCCCTCCCGCCTGCCCAACCAGTGTGTCCTCTGCAGCTG 817
    |||   :::   |||                 :::|||::::::|||:::||
785 HisProPheValProProPheGlyTyrIleLysCysAlaValCysThrCy 801

818 C......ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAAC 861
      |      :::   |||::::::::::|||      :::|||||||||
801 sLysGlySerThrGlyGluValHisCysGluLysValThrCysProProL 818

862 CAGGCTGCCCAGCACCCCTCCCGCTG...CCAGACTCCTGCTGCCAAGCC 908
        |||     |||:::          |||::::::|||||||:::
818 euThrCysSerArgProIleArgArgAsnProSerAspCysCysLysGlu 834

909 TGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTC 958
    |||     |||   :::          :::::::|||:::   :::|||::
835 CysProProGluGluThrProProLeuGluAspGluGluMetMetGlnAl 851
```

FIG. 13 (CONT.[1])

```
959 GCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGA 1008
                                  :
851 a..................................................  851

1009 GAAAGAGAGGCCCGGGCACCCCAGCCCCCACTGGCCTCAGCGCCCCTCTG 1058
                                  ||||||
852 ..........AspGlyThr.....................................  854

1059 AGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACTGT 1108
854 ..................................................  854

1109 CAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGGA 1158
                    :::   |||      |||   :
855 ..........................ArgLeuCysLysPheGlyLysA 862

1159 AGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC 1208
     ::   |||::::::::::|||   |||||||-||:::              |||
862 snTyrTyrGlnAsnSerGluHisTrpHisProSerValProLeuValGly 878
```

FIG. 13 (CONT.[2])

```
1209 CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCA 1258
      :::   ||||||   |||   |||:::   |||         |||||
 879 GluMetLysCysIleThrCysTrpCysAspHisGlyValThrLysCysGl 895

1259 GCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTCACCCCGAGAAAGTGG 1308
      ||||     ||||||              ||||||:::|||   ::::::
 895 nArgLysGlnCysProLeu...LeuSerCysArgAsnProIleArgThrG 911

1309 CTGGGAAGTGCTGCAAGATTTGCCCAGAGGAC 1340
      ||||||||||||      |||   ||||||
 911 luGlyLysCysCysProGluCysIleGluAsp 921
```

FIG. 13 (CONT.[3])

```
462 GGTTTGCCAGGCCCAGACATGTTCTGCCTTTTCCATGGGAAGAGATACTC 511
      |||   |||                    |||:::|||:::|||::::::
543 GlyArgProArgAspProAsnThrCysPhePheGluGlyGlnGlnArgPr 559

512 CCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGTACT 561
      |||      |||   |||      :::|||                   |
559 oHisGlyAlaArgTrpAlaProAsnTyrAspPro.............LeuC 572

562 GCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTC 611
    ||      |||||||||:::::   :::   |||   |||      :::
572 ysSerLeuCysThrCysGlnArgArgThr...ValIleCysAspProVal 587

612 CACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG 661
      |||||||||     |||||:::||||||      |||:::|||||
588 ValCysProProProSerCysProHisProValGlnAlaProAspGlnCy 604

662 CTGTCCCAAGTGTGTGGAA.....................CCTCACACTC 690
    |||||||   |||   |||                    |||      |
604 sCysProValCysProGluLysGlnAspValArgAspLeuProGlyLeuP 621
```

FIG. 14

```
691 CCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATG 740
      ||   :::   |||   |||   ::::::|||      :::|||
621 roArgSer...ArgAspProGlyGluGlyCysTyrPheAspGlyAspArg 636

741 TACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCT 790
        ::::::                  |||   :::   |||
637 SerTrpArgAlaAlaGlyThrArgTrpHisProValValProProPheGl 653

791 GCCCAACCAGTGTGTCCTCTGCAGCTGCACA......GAGGGCCAGATCT 834
      :::|||::::::|||:::|||                |||:::::::
653 yLeuIleLysCysAlaValCysThrCysLysGlyGlyThrGlyGluValH 670

835 ACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCG 884
     ::|||      :::   ||||||:::   :::|||      |||:::
670 isCysGluLysValGlnCysProArgLeuAlaCysAlaGlnProValArg 686

885 CTG...CCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCA 931
           :::   |||   :::|||||:::   |||
687 ValAsnProThrAspCysCysLysGlnCys..................  696
```

FIG. 14 (CONT.[1])

```
932 ATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTC 981
                    :::   :::      |||||||
697 ........................ProValGlySerGlyAlaHisProG 705

982 AG......GATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGC 1025
      ||      ||||||   :::::::|||                |||||
705 lnLeuGlyAspProMetGlnAlaAsp..............GlyPro... 715

1026 ACCCCAGCCCCCACTGGCCTCAGCGCCCCTCTGAGCTTCATCCCTCGCCA 1075
 715 ..................................................  715

1076 CTTCAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGG 1125
 715 ..................................................  715

1126 AGAAACATAAGAAAGCCTGTGTGCATGGCGGGAAGACGTACTCCCACGGG 1175
          :::::::|||      :::|||:::   :::   ::::::
 716 ..........ArgGlyCysArgPheAlaGlyGlnTrpPheProGluSer 728
```

FIG. 14 (CONT.^{2})

```
1176 GAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCTTGCCCTGCATCCT 1225
      :::   |||||||||:::          ||||||   :::   ||||||
 729 GlnSerTrpHisProSerValProProPheGlyGluMetSerCysIleTh 745

1226 ATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCA 1275
       |||   |||      |||          |||:::|||      |||
 745 rCysArgCysGlyAlaGlyValProHisCysGluArgAspAspCysSerL 762

1276 CCGAGTACCCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAG 1325
           |||          ::::::      ::::::||||||:::
 762 euProLeuSerCysGlySerGlyLysGlu......SerArgCysCysSer 776

1326 ATTTGC.....................CCAGAGGACAAAGCAGACCCT 1352
       |||                       ||||||   ::::::||||||
 777 ArgCysThrAlaHisArgArgProAlaProGluThrArgThrAspPro 792
```

FIG. 14 (CONT.[3])

```
243 GAGACAGTGGCATGCCCAGTGTTGCACAGTAAGTGTGTGGTAAAGCCGAG 292
    :::   |||   ||||||:::|||                :::|||:::|||::
724 AspProValMetCysProThrLeuSerCysThrHisThrValGlnProGl 740

293 ATTCAAACTCAGACCTTCTGGCCCCTTGCCTAGGAGAGCATGCCCAGTTG 342
    :                                    ::::::||||||:::
740 u.............................AspGlnCysCysProIle. 746

343 TCTAGCAGATTCTCTTTTGCCTGAGTGGCCCAGATGACATCTCTTTTAGA 392
        +++             |||   :::      ::::::   :::
747 ................CysGluGluLysLysGluSerLysGluThrAla 757

393 GCTAGAAAGAAGGAGAAATGAGACAGGGTCTTTGGGCTGGAGCCTCCTGG 442
    |||   :::|||   :::+++                      :::|||   ||
758 AlaValGluLysValGlu..................GluAsnProGluGl 768

443 GACTAACATGGCACTGGTCGGTTTGCCAGGCCCAGACATGTTCTGCCTTT 492
    |                                                |||   |
768 y.....................................CysTyrP 771

493 TCCATGGG......AAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTAC 536
    ||:::|||      |||   ::::::||||||   :::||||||||||:::
771 heGluGlyAspGlnLysMetHisAlaProGlyThrThrTrpHisProPhe 787
```

FIG. 15

```
537 TTGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGC...TCAGA 583
    :::   |||   |||   :::   |||       |||||||||   :::::
788 ValProProPheGlyTyrIleLysCysAlaValCysThrCysLysGlySe 804

584 GGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTCCACTGCC 633
    :   ::::::|||   |||   ::::::   |||||||||:::   |||
804 rThrGlyGluValHisCysGluLysValThrCysProProLeuThrCysS 821

634 CCCAGCCTGTG...ACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAA 680
        :::|||:::       :::|||::::::||||||   :::|||
821 erArgProIleArgArgAsnProSerAspCysCysLysGluCysProPro 837

681 CCTCACACTCCC.............................TCTGGACT 700
      :::||||||                                :::|||
838 GluGluThrProProLeuGluAspGluGluMetMetGlnAlaAspGlyTh 854

701 CCGGGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATGTACCAACACG 750
    |||                |||:::   :::   :::   ||||||::::
854 rArgLeu............CysLysPheGlyLysAsnTyrTyrGlnAsnS 867

751 GAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCTGCCCAACCAG 800
    ::|||   :::      |||         |||                :::
867 erGluHisTrp......HisProSerValProLeuValGlyGluMetLys 881
```

FIG. 15 (CONT.[1])

```
801 TGTGTCCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAAC 850
          |||:::   |||   |||   :::|||          |||
882 CysIleThrCysTrpCysAspHisGlyValThrLysCysGlnArgLysGl 898

851 CTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCGCTGCCAGACTCCTGCT 900
    ||||||      :::|||      |||:::                :::||||
898 nCysProLeuLeuSerCysArgAsnProIleArgThrGluGlyLysCysC 915

901 GCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGT 950
          ||     |||   ::::::      |||::::::::::
915 ysProGluCysIleGluAspPheMetGluLysGluGluMetAlaLysMet 931

951 GTGCAGTCGCTCCATGGGGTGAGACAT 977
    :::::::::      :::   ||||||
932 AlaGluLysLysLysSerTrpArgHis 940
```

FIG. 15 (CONT.^{2})

```
462 GGTTTGCCAGGCCCAGACATGTTCTGCCTTTTCCATGGGAAGAGATACTC 511
      |||   |||                  |||:::|||:::|||::::::
543 GlyArgProArgAspProAsnThrCysPhePheGluGlyGlnGlnArgPr 559

512 CCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGTACT 561
      |||      |||   |||      :::|||                  |
559 oHisGlyAlaArgTrpAlaProAsnTyrAspPro.............LeuC 572

562 GCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTC 611
    ||      |||||||||::::::   :::   |||   |||      :::
572 ysSerLeuCysThrCysGlnArgArgThr...ValIleCysAspProVal 587

612 CACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG 661
      |||||||||      ||||||::::||||||      |||:::|||||
588 ValCysProProProSerCysProHisProValGlnAlaProAspGlnCy 604

662 CTGTCCCAAGTGTGTGGAA.....................CCTCACACTC 690
    |||||||   |||   |||                     |||      |
604 sCysProValCysProGluLysGlnAspValArgAspLeuProGlyLeuP 621
```

FIG. 16

```
691 CCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATG 740
       ||   :::   |||   |||   :::::::|||       :::|||
621 roArgSer...ArgAspProGlyGluGlyCysTyrPheAspGlyAspArg 636

741 TACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCT 790
          ::::::                    |||   :::   |||
637 SerTrpArgAlaAlaGlyThrArgTrpHisProValValProProPheGl 653

791 GCCCAACCAGTGTGTCCTCTGCAGCTGCACA......GAGGGCCAGATCT 834
       :::|||:::::::|||:::|||                |||:::::::
653 yLeuIleLysCysAlaValCysThrCysLysGlyGlyThrGlyGluValH 670

835 ACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCG 884
     ::|||      :::   ||||||:::   :::|||      |||:::
670 isCysGluLysValGlnCysProArgLeuAlaCysAlaGlnProValArg 686

885 CTG...CCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCA 931
             :::   |||   :::|||||:|:::   |||
687 ValAsnProThrAspCysCysLysGlnCys..................... 696
```

FIG. 16 (CONT.[1])

```
932 ATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTC 981
                  :::   :::      |||||||
697 ........................ProValGlySerGlyAlaHisProG 705

        982 AG......GATCCATGTTCCAGTGATGCTGGGAGA 1010
             ||      ||||||   ::::::|||:::   |||
         705 lnLeuGlyAspProMetGlnAlaAspGlyProArg 716
```

FIG. 16 (CONT.^{2})

```
243 GAGACAGTGGCATGCCCAGTGTTGCACAGTAAGTGTGTGGTAAAGCCGAG 292
    :::   |||   ||||||:::|||              :::|||:::|||::
724 AspProValMetCysProThrLeuSerCysThrHisThrValGlnProGl 740

293 ATTCAAACTCAGACCTTCTGGCCCCTTGCCTAGGAGAGCATGCCCAGTTG 342
    :                                    ::::::||||||:::
740 u.............................AspGlnCysCysProIle. 746

343 TCTAGCAGATTCTCTTTTGCCTGAGTGGCCCAGATGACATCTCTTTTAGA 392
        +++                 |||   :::      ::::::   :::
747 ..................CysGluGluLysLysGluSerLysGluThrAla 757

393 GCTAGAAAGAAGGAGAAATGAGACAGGGTCTTTGGGCTGGAGCCTCCTGG 442
    |||   :::|||   :::+++                        :::|||   ||
758 AlaValGluLysValGlu.....................GluAsnProGluGl 768

443 GACTAACATGGCACTGGTCGGTTTGCCAGGCCCAGACATGTTCTGCCTTT 492
    |                                                |||   |
768 y.....................................CysTyrP 771
```

FIG. 17

```
493 TCCATGGG......AAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTAC 536
    ||:::|||       |||   ::::::||||||   :::||||||||:::
771 heGluGlyAspGlnLysMetHisAlaProGlyThrThrTrpHisProPhe 787

537 TTGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGC...TCAGA 583
    :::   |||   |||   :::   |||       |||||||||   :::::
788 ValProProPheGlyTyrIleLysCysAlaValCysThrCysLysGlySe 804

584 GGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTCCACTGCC 633
     :   :::::::|||.  |||   ::::::   |||||||||:::   |||
804 rThrGlyGluValHisCysGluLysValThrCysProProLeuThrCysS 821

634 CCCAGCCTGTG...ACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAA 680
        :::|||:::      :::|||:::::::||||||   :::|||
821 erArgProIleArgArgAsnProSerAspCysCysLysGluCysProPro 837

681 CCTCACACTCCC.....................................TCTGGACT 700
      :::||||||                                     :::|||
838 GluGluThrProProLeuGluAspGluGluMetMetGlnAlaAspGlyTh 854
```

FIG. 17 (CONT.[1])

```
701 CCGGGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATGTACCAACACG 750
    |||                |||:::   :::   :::   ||||||::::
854 rArgLeu............CysLysPheGlyLysAsnTyrTyrGlnAsnS 867

751 GAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCTGCCCAACCAG 800
    ::|||   :::      |||         |||                :::
867 erGluHisTrp......HisProSerValProLeuValGlyGluMetLys 881

801 TGTGTCCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAAC 850
        |||:::   |||   |||   :::|||          |||
882 CysIleThrCysTrpCysAspHisGlyValThrLysCysGlnArgLysGl 898

851 CTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCGCTGCCAGACTCCTGCT 900
    ||||||      :::|||     |||:::              :::||||
898 nCysProLeuLeuSerCysArgAsnProIleArgThrGluGlyLysCysC 915

901 GCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGT 950
        ||      |||   ::::::     |||:::::::::
915 ysProGluCysIleGluAspPheMetGluLysGluGluMetAlaLysMet 931

951 GTGCAGTCGCTCCATGGGGTGAGACAT 977
    :::::::::      :::   ||||||
932 AlaGluLysLysLysSerTrpArgHis 940
```

FIG. 17 (CONT.^{2})

```
462 GGTTTGCCAGGCCCAGACATGTTCTGCCTTTTCCATGGGAAGAGATACTC 511
      |||   |||                     |||:::|||:::|||::::::
543 GlyArgProArgAspProAsnThrCysPhePheGluGlyGlnGlnArgPr 559

512 CCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGTACT 561
     |||      |||   |||      :::|||                  |
559 oHisGlyAlaArgTrpAlaProAsnTyrAspPro............LeuC 572

562 GCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTC 611
    ||      |||||||||::::::   :::   |||  |||       :::
572 ysSerLeuCysThrCysGlnArgArgThr...ValIleCysAspProVal 587

612 CACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG 661
     |||||||||       ||||||:::||||||      |||:::|||||
588 ValCysProProProSerCysProHisProValGlnAlaProAspGlnCy 604

662 CTGTCCCAAGTGTGTGGAA...................CCTCACACTC 690
    |||||||   |||  |||               .       |||      |
604 sCysProValCysProGluLysGlnAspValArgAspLeuProGlyLeuP 621
```

FIG. 18

```
691 CCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATG 740
      ||   :::   |||   |||   :::::::|||      :::|||
621 roArgSer...ArgAspProGlyGluGlyCysTyrPheAspGlyAspArg 636

741 TACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCT 790
        ::::::                  |||   :::   |||
637 SerTrpArgAlaAlaGlyThrArgTrpHisProValValProProPheGl 653

791 GCCCAACCAGTGTGTCCTCTGCAGCTGCACA......GAGGGCCAGATCT 834
     :::|||::::::|||:::|||            |||:::::::
653 yLeuIleLysCysAlaValCysThrCysLysGlyGlyThrGlyGluValH 670

835 ACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCG 884
     ::|||      :::   ||||||:::   :::|||      |||:::
670 isCysGluLysValGlnCysProArgLeuAlaCysAlaGlnProValArg 686

885 CTG...CCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCA 931
           :::   |||   :::|||||:|:::   |||
687 ValAsnProThrAspCysCysLysGlnCys..................... 696
```

FIG. 18 (CONT.[1])

```
932 ATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTC 981
                  :::   :::      |||||||
697 ........................ProValGlySerGlyAlaHisProG 705

       982 AG......GATCCATGTTCCAGTGATGCTGGGAGA 1010
            ||      ||||||   :::::::|||:::   |||
        705 lnLeuGlyAspProMetGlnAlaAspGlyProArg 716
```

FIG. 18 (CONT.^{2})

```
cdinLM_var1    1 TFPLSLIASPFCWTFLRLSISPSFPRVLFPPFSSSHLRPPFLPSFPAHRCFLALLRPRSS
cdinLM_var2    1 TFPLSLIASPFCWTFLRLSISPSFPRVLFPPFSSSHLRPPFLPSFPAHRCFLALLRPRSS
cdinLM_var4    1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
cdinLM_var5    1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
cdinLM_var3    1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
cdinLM_var6    1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

cdinLM_var1   61 SRPPGVCGLICGPCASVSFSSPFLPTPLPDQRPDPGERMVPEVRVLSSELGLALLWFPED
cdinLM_var2   61 SRPPGVCGLICGPCASVSFSSPFLPTPLPDQRPDPGERMVPEVRVLSSLLGLALLWFPLD
cdinLM_var4    1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~DRVFGLEPPGTNMA
cdinLM_var5    1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~DRVFGLEPPGTHMA
cdinLM_var3    1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
cdinLM_var6    1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~DRVFGLEPPGTNMA

cdinLM_var1  121 SHARAR[illegible]
cdinLM_var2  121 SHARAR[illegible]
cdinLM_var4   15 [illegible]
cdinLM_var5   15 [illegible]
cdinLM_var3    1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~IS[illegible]W[illegible]QMQNHQKSGLVNFSKD
cdinLM_var6   15 [illegible]
```

FIG. 19

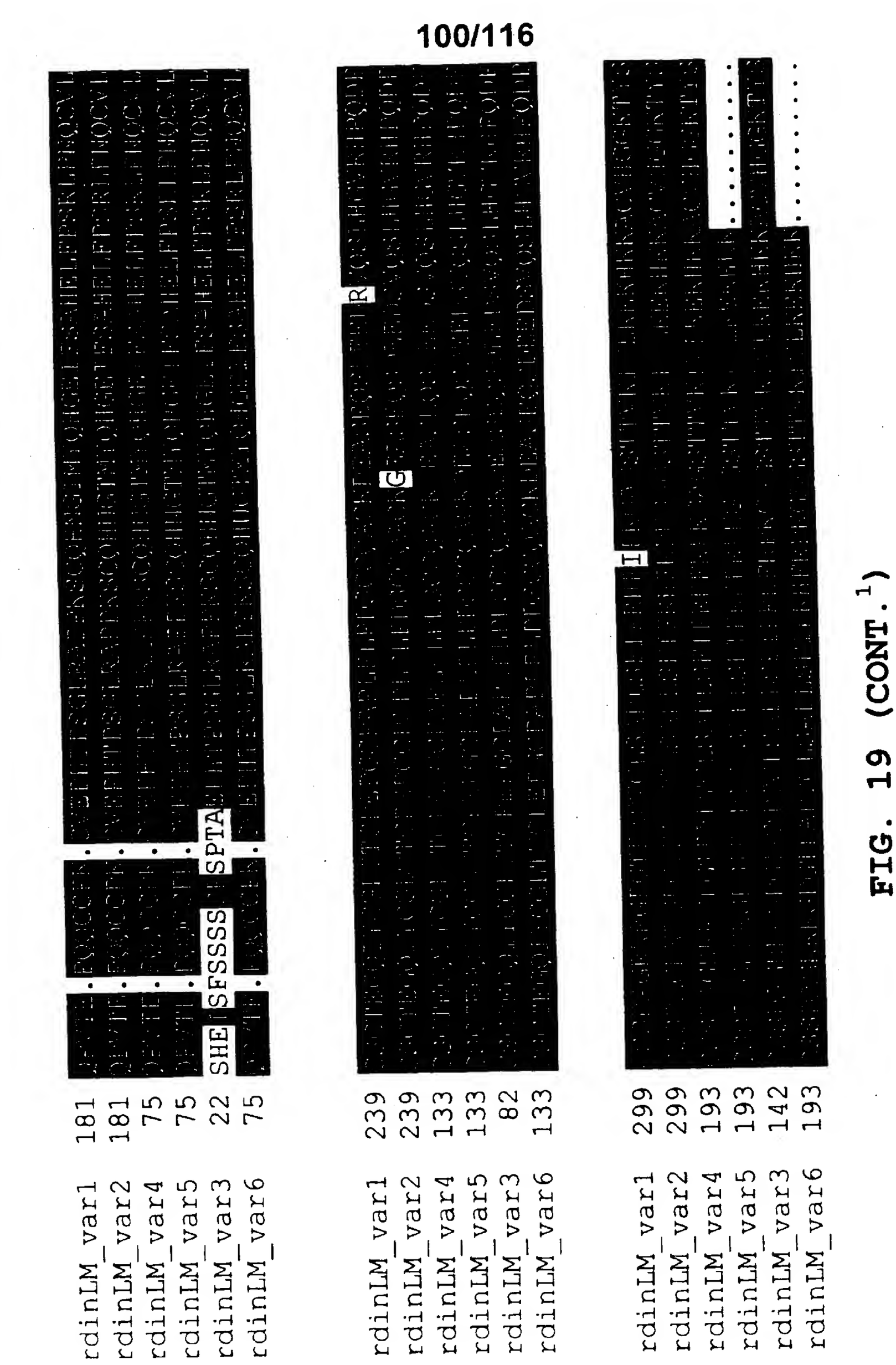
rdinLM_var1 181
rdinLM_var2 181
rdinLM_var4 75
rdinLM_var5 75
rdinLM_var3 22
rdinLM_var6 75
rdinLM_var1 239
rdinLM_var2 239
rdinLM_var4 133
rdinLM_var5 133
rdinLM_var3 82
rdinLM_var6 133
rdinLM_var1 299
rdinLM_var2 299
rdinLM_var4 193
rdinLM_var5 193
rdinLM_var3 142
rdinLM_var6 193

FIG. 19 (CONT.[1])

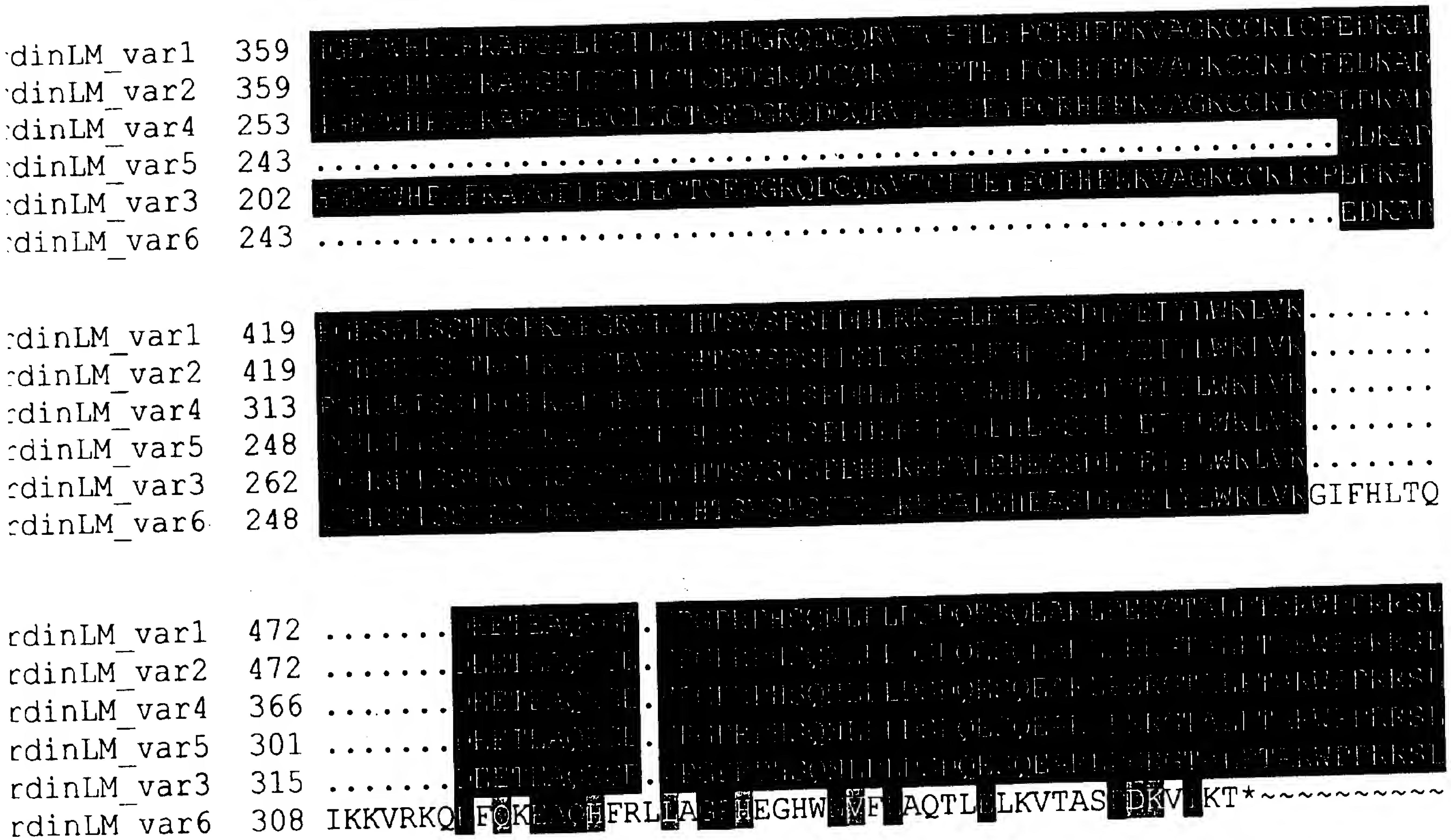
rdinLM_var1 359
rdinLM_var2 359
rdinLM_var4 253
rdinLM_var5 243
rdinLM_var3 202
rdinLM_var6 243
rdinLM_var1 419
rdinLM_var2 419
rdinLM_var4 313
rdinLM_var5 248
rdinLM_var3 262
rdinLM_var6 248
GIFHLTQ
rdinLM_var1 472
rdinLM_var2 472
rdinLM_var4 366
rdinLM_var5 301
rdinLM_var3 315
rdinLM_var6 308
IKKVRKQ
AQTL
LKVTAS
KT*

FIG. 19 (CONT.[2])

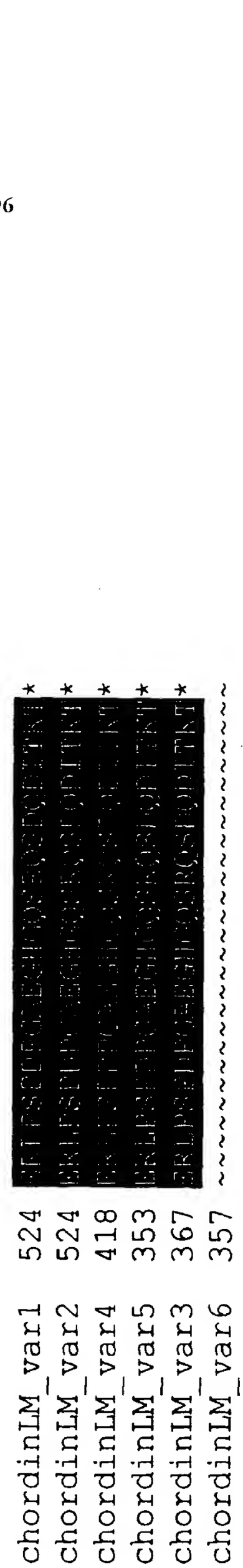
chordinLM_var1
chordinLM_var2
chordinLM_var4
chordinLM_var5
chordinLM_var3
chordinLM_var6
524
524
418
353
367
357

FIG. 19 (CONT.3)

```
425 AGACATTCC...............CAGGATCCATGCTCGGAGAGGAGAGG 459
    |||||||||                |||||      :::|||:::::
  1 ArgHisSerTyrHisArgSerHisTyrAspProProProSerArgGlnAl 17

460 CCCCAGCACGCCAGCCCCCACCAGCCTCAGCTCCCCTCTGGGCTTCATCC 509
    :   :::                :::      |||      |||   :::
 17 aGlyGlyLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeuM 34

510 NTCGCCACTTCCAGTCAGTAGGAATGGGCAGCACAACCATCAAGATTATC 559
        |||:::  |||          |||   ::::::|||:::
 34 etAspSerGlnGlnAlaSerGly.........ThrIleValGlnIleVal 47

560 TTGAAGGAGAAACATAAA......AAAGCTTGCACACACAATGGGAAGAC 603
    ::::::::::|||||||||      ::::::|||:::   ||||||||||
 48 IleAsnAsnLysHisLysHisGlyGlnValCysValSerAsnGlyLysTh 64

604 ATACTCCCATGGGGAGGTGTGGCACCCCACTGTGCTCTCCTTTGGCCCCA 653
    ||||||||||||||||   |||||||||:::::   :::||||||   :
 64 rTyrSerHisGlyGluSerTrpHisProAsnLeuArgAlaPheGlyIleV 81
```

FIG. 20

```
654 TGCCCTGCATCCTGTGCACATGTATTGATGGCTACCAGGACTGCCACCGT 703
    ::   |||:::|||||||||||||||          |||:::|||   :::
 81 alGluCysValLeuCysThrCysAsnValThrLysGlnGluCysLysLys 97

704 GTGACCTGCCCCACCCAATATCCCTGCAGTCAACCCAAGAAAGTGGCTGG 753
    :::   ||||||::::::|||||||||:::   |||:::|||:::   ||
 98 IleHisCysProAsnArgTyrProCysLysTyrProGlnLysIleAspGl 114

754 GAAGTGCTGCAAGATCTGCCCAGAGGACGAGGCGGAAGATGACCACAGTG 803
        ||||||||||||||::||||||      :::|||:::::::::
114 yLysCysCysLysValCysProGlyLysLysAlaLysGluGlu..... 128

804 AGGTCATTTCCACCCGGTGTCCCAAGGTACCAGGCCAG..... 841
                        :::|||||||||
129 .........................LeuProGlyGlnSerPheAspAsn 136

842 .........................TTCCAGGTGTAC...ACGTTGGC 861
                     :::   ||||||   ::::::
137 LysGlyTyrPheCysGlyGluGluThrMetProValTyrGluSerValPh 153
```

FIG. 20 (CONT.[1])

```
862 ATCTCCAAGCCCAGACAGCCTACACCGCTTTGTCCTGGAGCATGAAGCCT 911
          :::   ::::::   :::::::::::::||||||   |||
153 eMetGluAspGlyGluThrThrArgLysIleAlaLeuGluThrGluArgP 170

912 CTGACCAGGTAGAGATGTACATTTGGAAGCTGGTGAAAGGAATTTACCAC 961
      ||||||||:::::::::|||   :::   ||||||||   :::
170 roProGlnValGluValHisValTrpThrIleArgLysGlyIleLeuGln 186

962 TTGGTTCAGATCAAGAGAGTCAGGAAGCAAGATTTCCAGAAAGAGGTTCA 1011
          :::|||:::::::::   |||:::   |||:::   |||:::
187 HisPheHisIleGluLysIleSerLysArgMetPheGlu...GluLeuPr 202

1012 GAACTTCCGGCTGCTCACCGGCACCCATGAAGGTTACTGGACCGTTTTCC 1061
       :::|||:::|||:::|||   |||       :::   |||   :::|||
202 oHisPheLysLeuValThrArgThrThrLeuSerGlnTrpLysIlePheT 219

1062 TA.........GCCCAGATTCCAGAGCTGAAAGTTACAGCCAGCCCAGAC 1102
           |||||||||   ::::::                      :::
219 hrGluGlyGluAlaGlnIleSerGlnMet.............CysSerSer 231
```

FIG. 20 (CONT.[2])

```
1103 AAAGTGACCAAGACATTATAGCAAGGACCTAAAGAGTTGCAGATAC 1152
     :::|||| ||    ::::|||| +++          |||||||:::
232  ArgValCysAsArgThr.....GluLeuGluAsp. 240

1153 TTTATTGGTTTTGTTATTATATTAATAAA 1183
     |||||||  :::|||||||:::::::::
241  ....LeuValLysValLeuTyrLeuGluArg 249
```

FIG. 20 (CONT.[3])

```
 18 CCCACACTGCTCTGCCTACCCACACCA...GCCCCAAGGTCTNAGAAAGC 64
     |||   |||   :::   |||   |||   ||||||      :::|||
673 ProMetLeuProAlaGlyProGlyProGluAlaProValProAlaLysHi 689

 65 CCTGGAGGCTGGCTTGCCA...AATCCTTGTCAGTGTNTTTATTGATTAG 111
       :::   |||   |||   :::|||      |||   :::+++
689 sGlySerProGlyArgProArgAspProAsnThrCysPhePhe..... 703

112 TCTGAGAATATCTTAGACCTCACCCACAAGGTTCTGTGTGGAGC..... 155
       +++          :::   :::|||:::|||:::   |||:::
704 ........GluGlyGlnGlnArgProHisGlyAlaArgTrpAlaProAsn 717

156 .........CTGTGCTCTCTGTCTGTCTGT.........CTGTCTGTCTG 187
        ||||||||||||   :::|||                :::||
718 TyrAspProLeuCysSerLeuCysIleCysGlnArgArgThrValIleCy 734

188 TCTGTCTGTCTGTCTGCCTGCCTCTCTCTGTCTGTCTCCGTCTGTCTCTG 237
        |     |||     |||     .   |||     |||
734 sAspProValValCysProProProSerCysProHisPro..... 747
```

FIG. 21

```
238 TCTCTCTGTCTGTCTCTGTCTG.TCTCTTTCTCTCTGTCTCTCTCTGTGT 286
          |||   :::|||:::   |||      :::|||
748 ................ValGlnAlaLeuAspGlnCysCysProValCys 758

287 CTCTGTCTCTGTCTCTGTCTCTCTCTCTCTCAGAAGTCCTCTAGCCTT 336
                            |||
759 ..................................ProGluLysGl 762

337 CTCTAGCAGGCGTCTC.............ATGCAGCCTGGT...TGGT 368
      ||||||   |||                :::::|||||      |
762 nArgSerArgAspLeuProSerLeuProAsnLeuGluProGlyGluGlyC 779

369 GT...........TCCCAGCTGTGGCCTATCCCACAGACAGCTCCACAT 406
    ||            ::::::  |||           |||     |||
779 ysTyrPheAspGlyAspArgSerTrpArgAlaAlaGlyThrArgTrpHis 795

407 CCT..............................GCTTGCTGTTC 420
    |||                             :::   |||::
796 ProValValProProPheGlyLeuIleLysCysAlaValCysThrCysLy 812
```

FIG. 21 (CONT.[1])

```
421 GCAGAGACATTCCCAGGATCCATGCTCGGAGAGGAGAGGCCCC..... 463
      :          ::::::      |||::::::   :::   |||
812 sGlyAlaThrGlyGluValHisCysGluLysValGlnCysProArgLeuA 829

464 ....................AGCACGCCAGCCCCCACCAGCCTCAGCTCC 493
                 ::::::|||:::             :::
829 laCysAlaGlnProValArgAlaAsnProThrAspCysCysLysGlnCys 845

494 CCTCTGGGCTTCATCCNTCGCCACTTCCAGTCAGTAGGAATGGGCAGCAC 543
    |||::::|||                          ::::::||
846 ProValGly.................................SerGlyTh 851

544 AACCATCAAGATT......ATCTTGAAGGAGAAACATAAAAAAGCTTGCA 587
     |:::   |||:::         ::::::          ::::::|||
851 rAsnAlaLysLeuGlyAspProMetGlnAlaAspGlyProArgGlyCysA 868

588 CACACAATGGGAAGACATACTCCCATGGGGAGGTGTGGCACCCCACTGTG 637
       |||:::   :::   :::::::::   ||||||||||::::|||
868 rgPheAlaGlyGlnTrpPheProGluAsnGlnSerTrpHisProSerVal 884
```

FIG. 21 (CONT.[2])

PCT/IL00/00736

09/890456

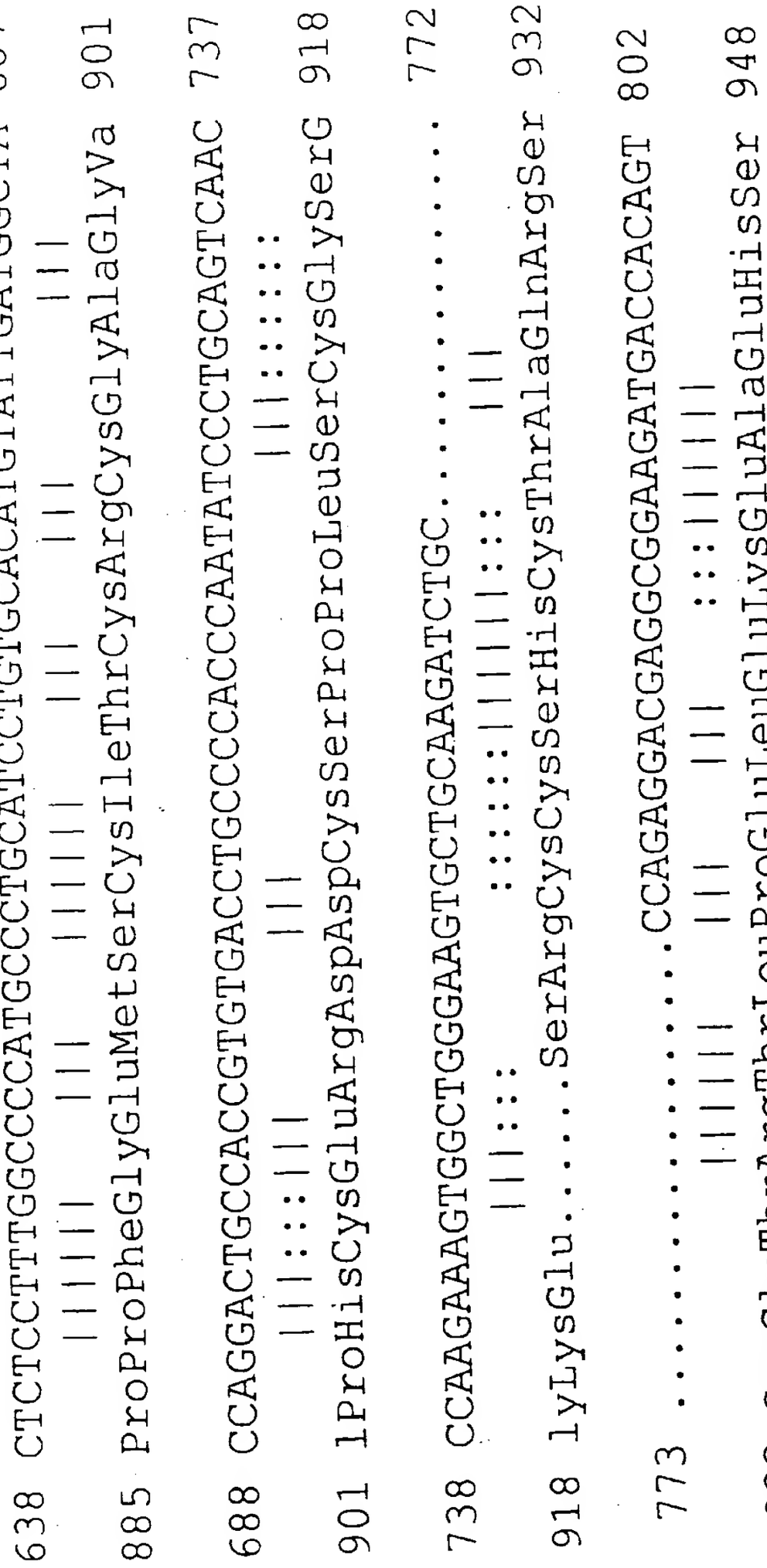
638 CTCTCCTTTGGCCCCATGCCCATGCCCTGCATCCTGTGCACATGTATTGATGGCTA 687
885 ProProPheGlyGluMetSerCysIleThrCysArgCysGlyAlaGlyVa 901
688 CCAGGACTGCCACCCGTGTGACCTGCCCCCACCCAATATCCCTGCAGTCAAC 737
901 lProHisCysGluArgAspCysSerProProLeuSerCysGlySerG 918
738 CCAAGAAGTGGCTGCAAGATCTGC..... 772
918 lyLysGlu..... 925
773 787
933 SerGluThrArgSerArgCysCysSerHisCysThrAlaGlnArgSer 932
802 CCAGAGGACGGAGGCGGAAGATGACCACAGT 802
948 GlnHisSer 948

FIG. 21 (CONT.3)

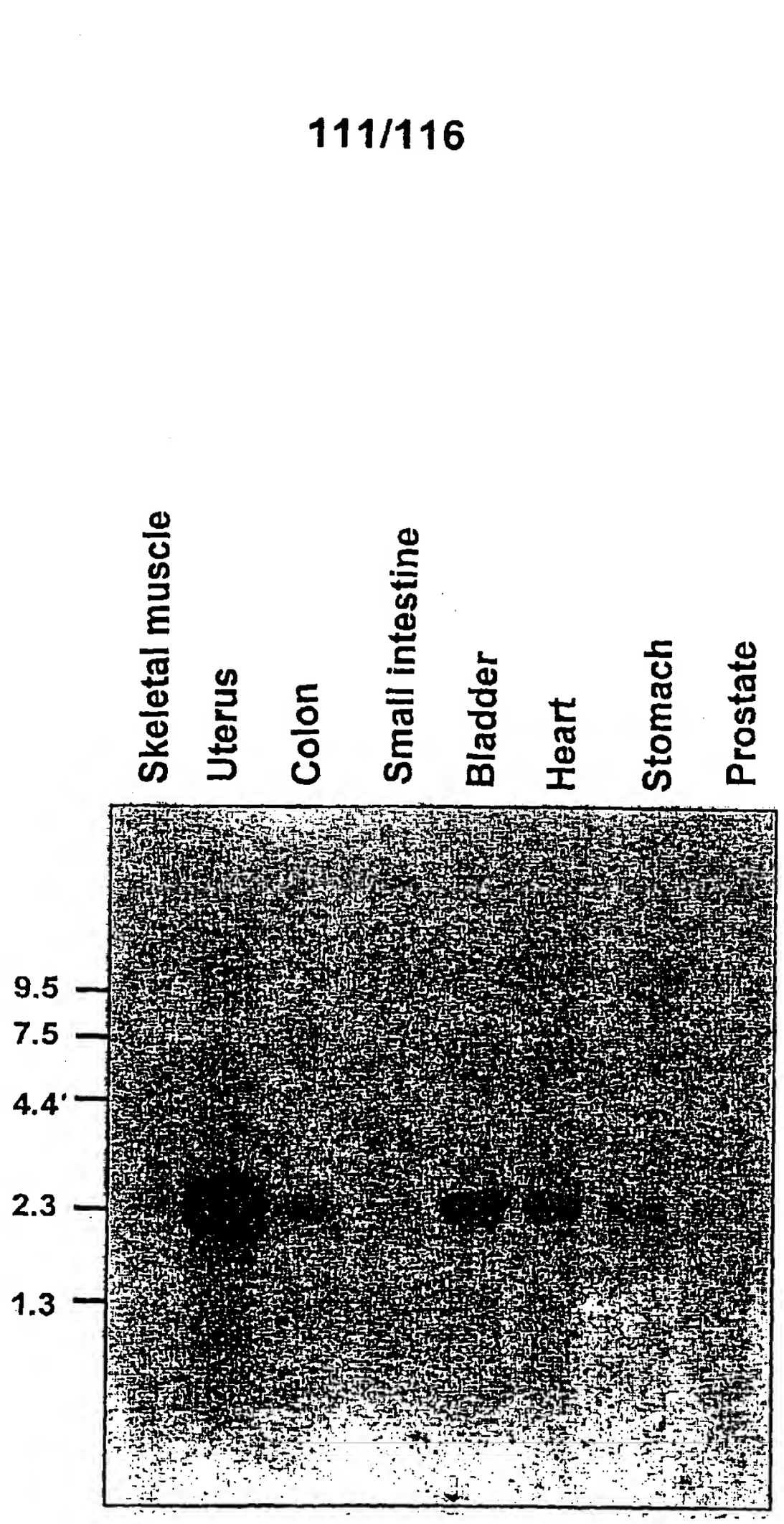
Skeletal muscle
Uterus
Colon
Small intestine
Bladder
Heart
Stomach
Prostate
9.5
7.5
4.4
2.3
1.3

Fig. 22

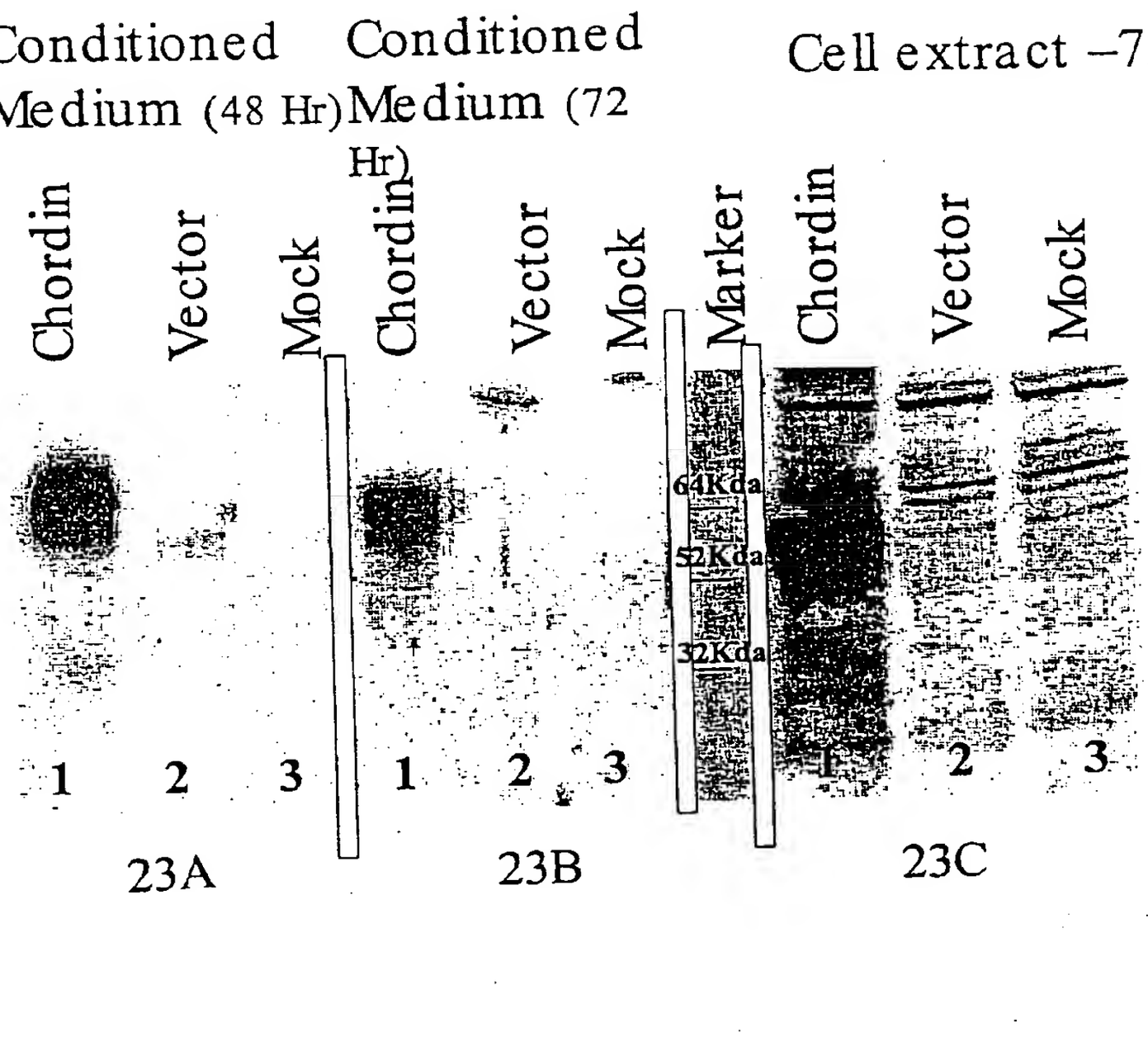
Conditioned Medium (48 Hr)
Conditioned Medium (72 Hr)
Cell extract –72Hr
Chordin
Vector
Mock
Chordin
Vector
Mock
Marker
Chordin
Vector
Mock
64Kda
52Kda
32Kda
1
2
3
1
2
3
2
3
23A
23B
23C

Fig. 23

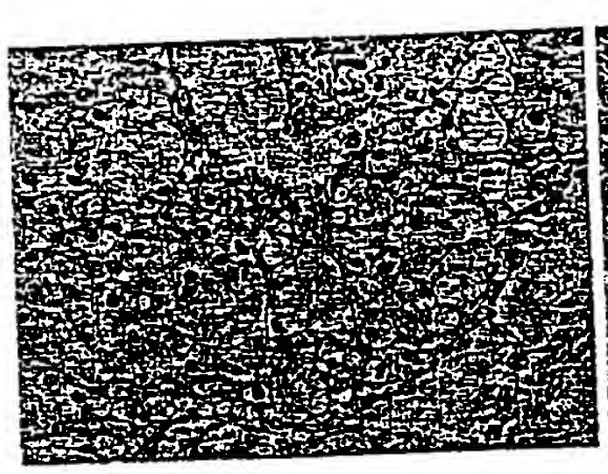

Fig.24A

Fig.24A'

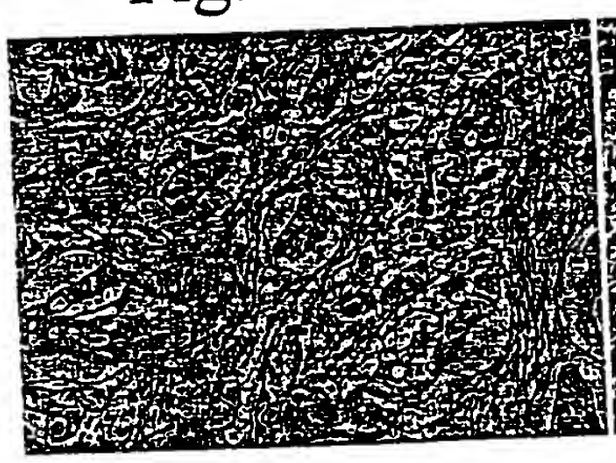

Fig.24B

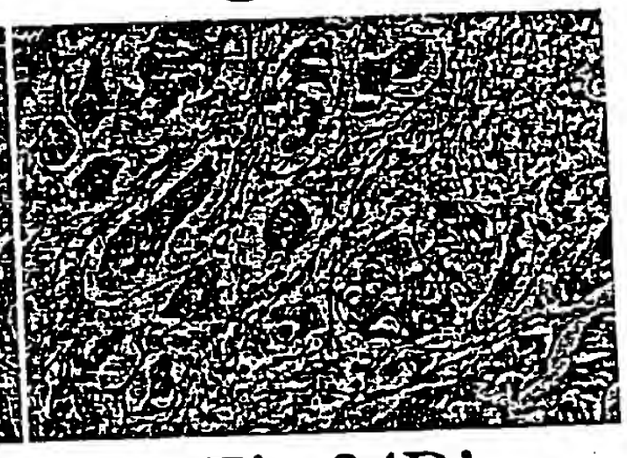

Fig.24B'

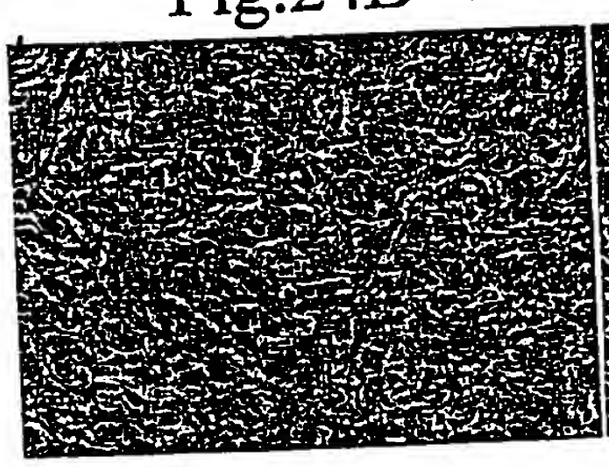

Fig.24C

Fig.24C'

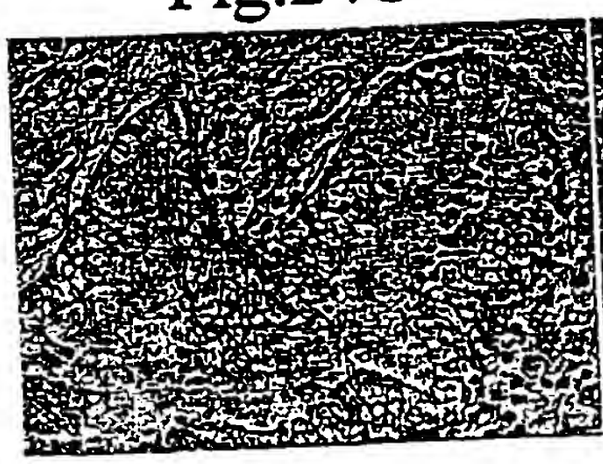

Fig.24D

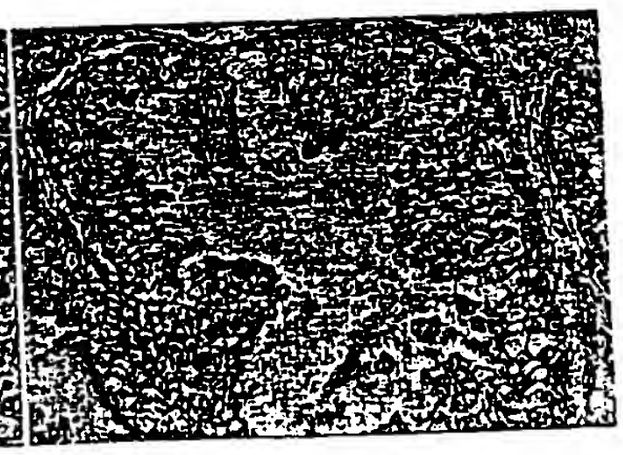

Fig.24D'

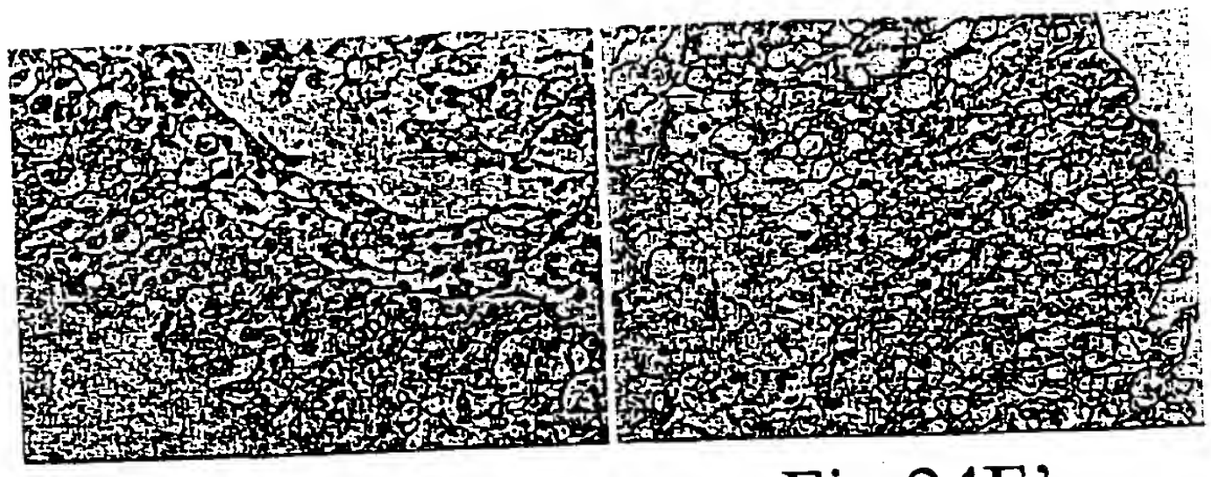

Fig.24E Fig.24E'

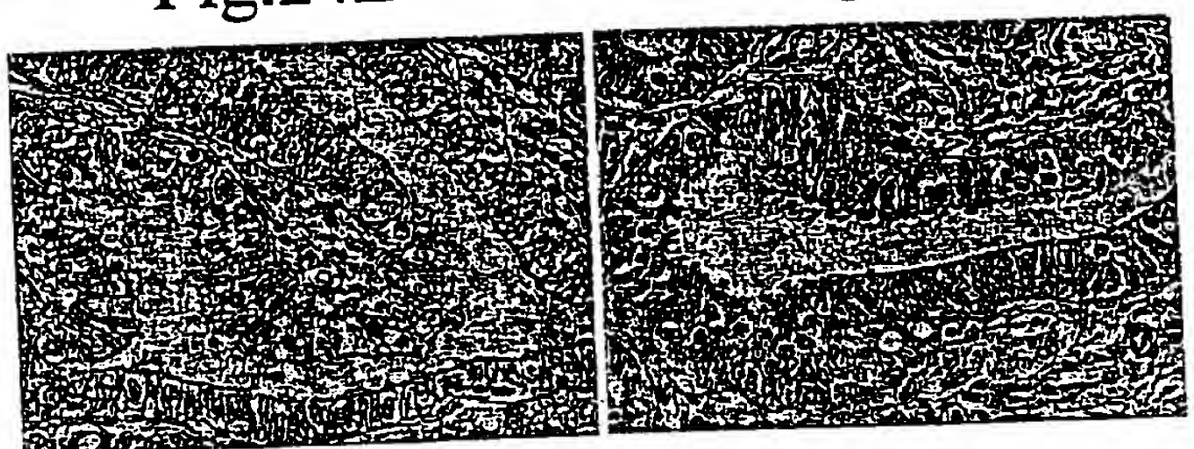

Fig.24F Fig.24F'

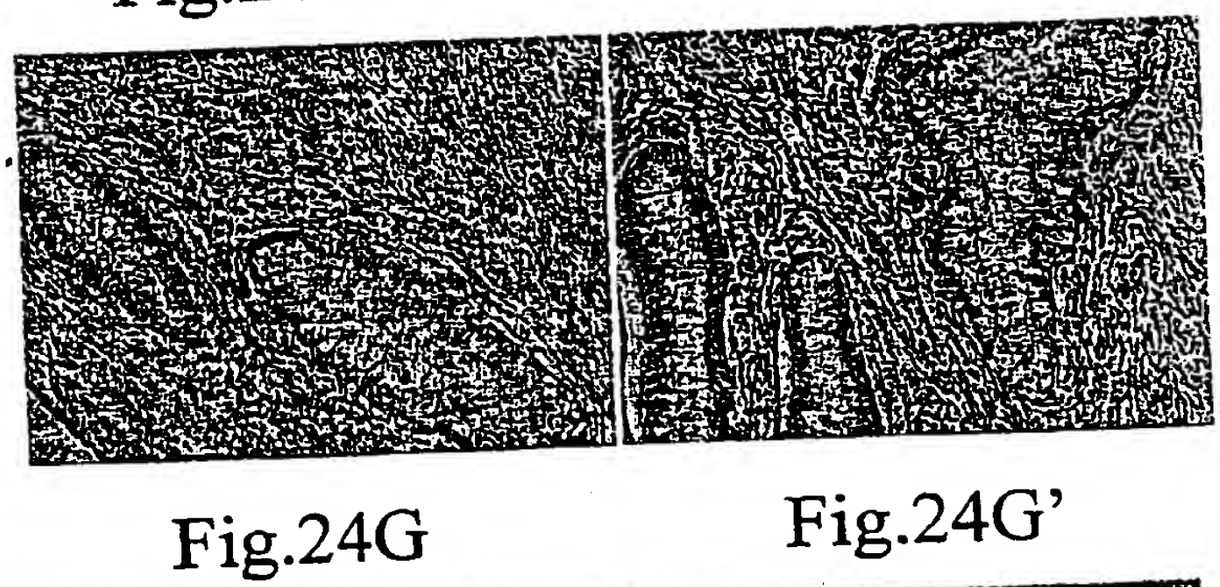

Fig.24G Fig.24G'

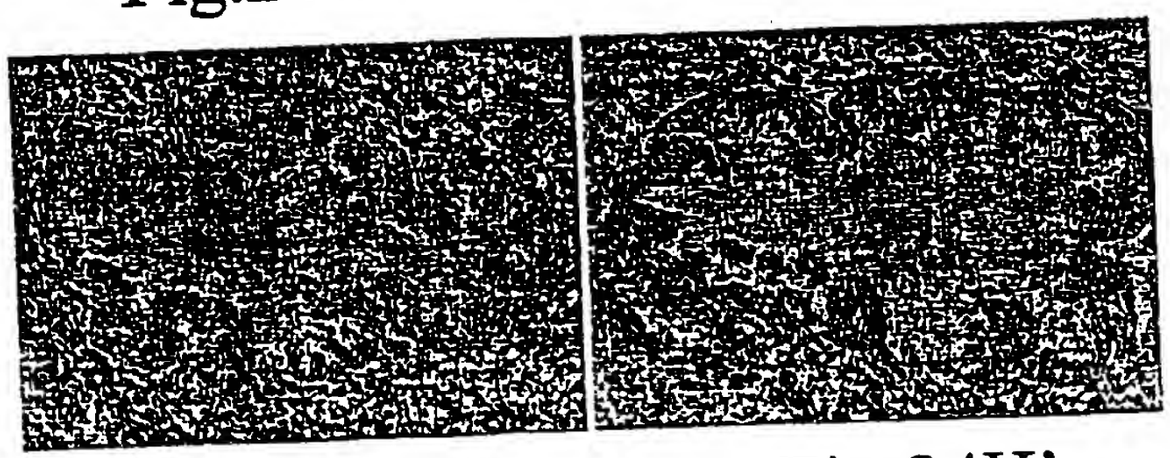

Fig.24H Fig.24H'

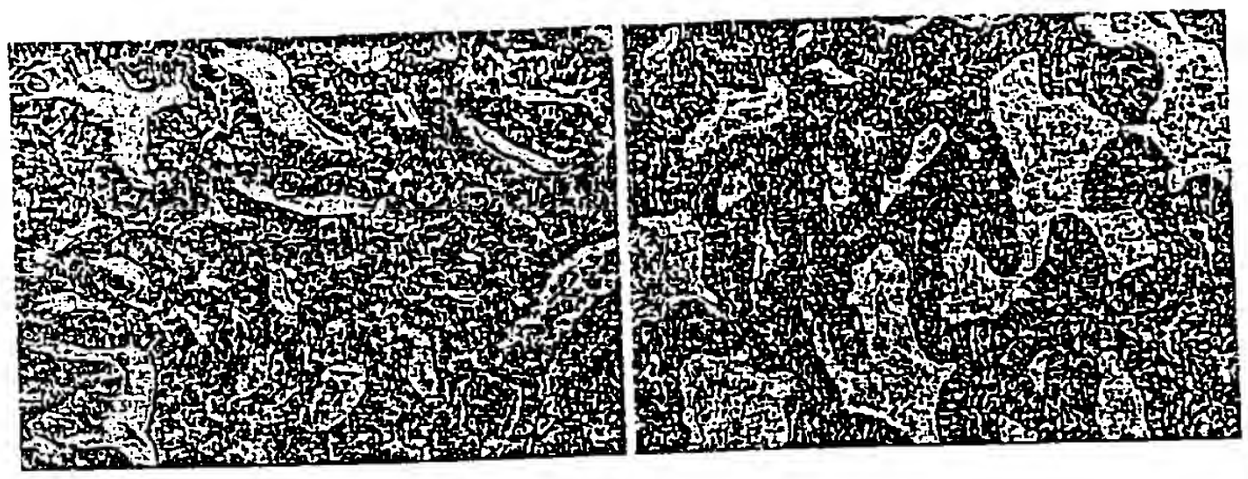

Fig.24I

Fig.24I'

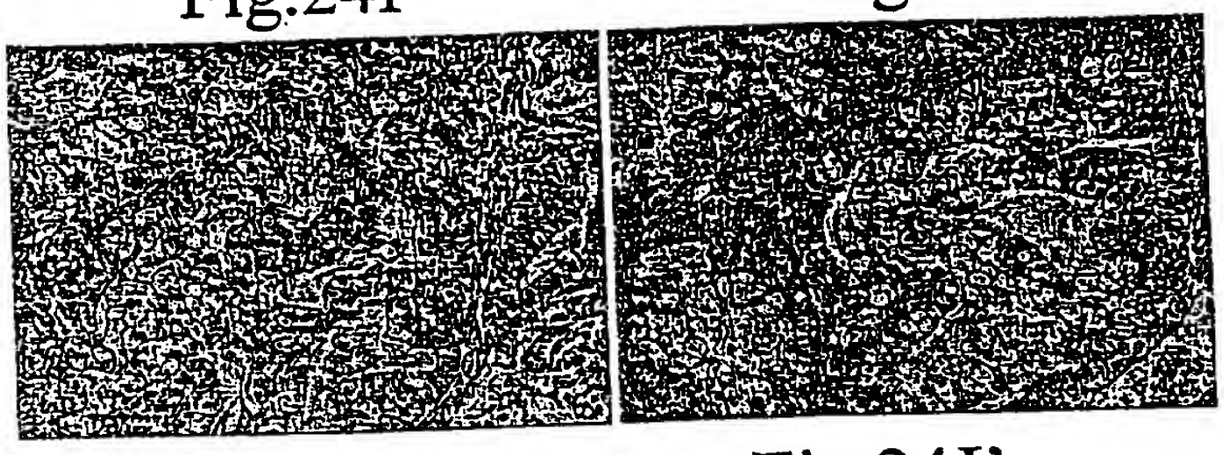

Fig.24J

Fig.24J'

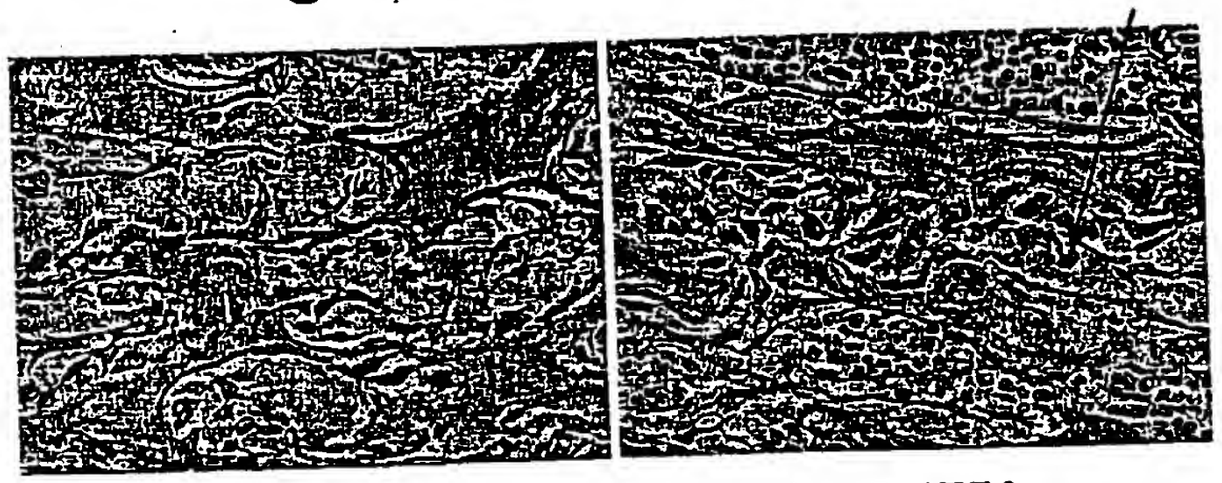

Fig.24K

Fig.24K'

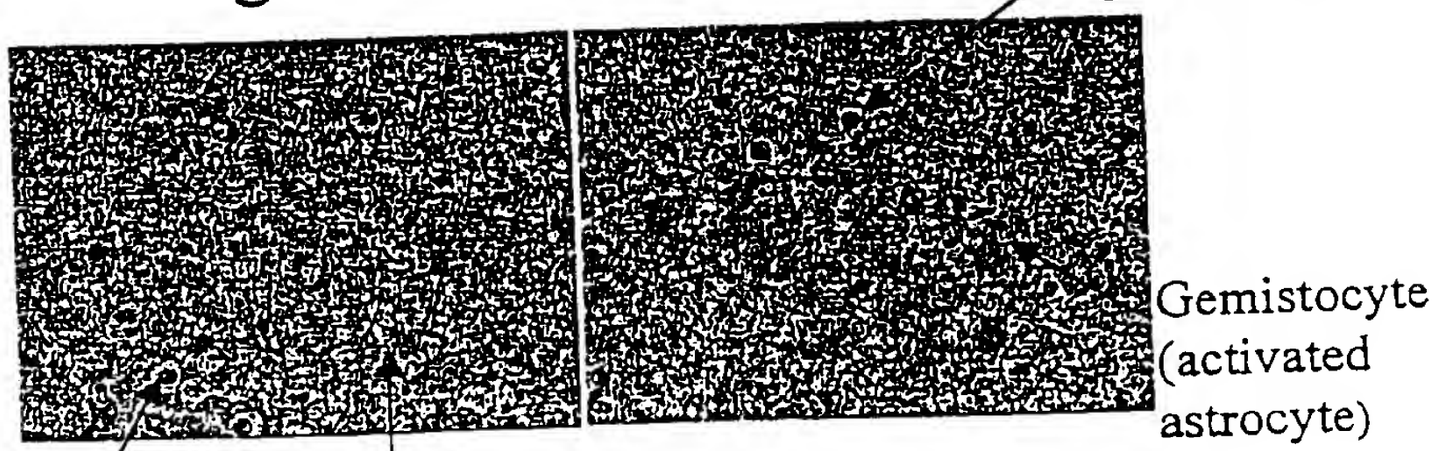

Fig.24L

Fig.24L'

25A

25B

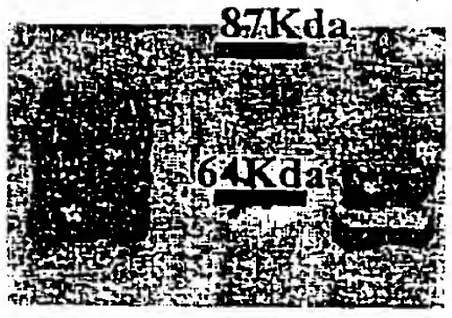

Fig. 25